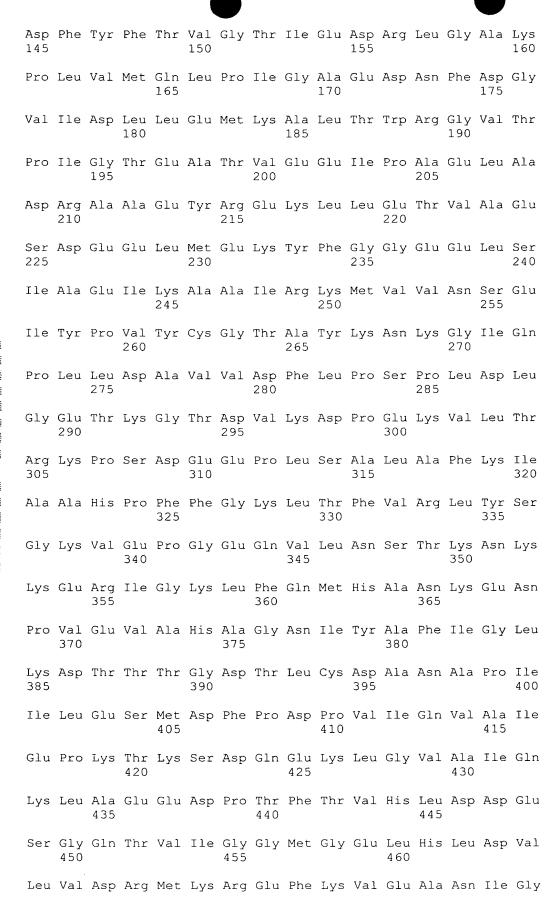
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465 470 475 480 Asp Pro Gln Val Ala Tyr Arg Glu Thr Ile Arg Lys Pro Val Glu Ser 485 490 Leu Ser Tyr Thr His Lys Lys Gln Thr Gly Gly Ser Gly Gln Phe Ala Lys Val Ile Ile Thr Ile Glu Pro Tyr Ala Pro Glu Ala Asp Glu Leu Glu Glu Gly Glu Ser Ala Ile Tyr Lys Phe Glu Asn Ala Val Thr Gly Gly Arg Val Pro Arg Glu Tyr Ile Pro Ser Val Asp Ala Gly Ile Gln 555 Asp Ala Met Gln Tyr Gly Phe Leu Ala Gly Tyr Pro Leu Val Asn Val 565 Lys Ala Thr Leu Glu Asp Gly Ala Tyr His Asp Val Asp Ser Ser Glu 585 Met Ala Phe Lys Leu Ala Gly Ser Gln Ala Phe Lys Glu Ala Val Ala 600 605 Lys Ala Lys Pro Val Leu Leu Glu Pro Ile Met Ser Val Glu Ile Thr 615 Thr Pro Glu Glu Tyr Met Gly Glu Val Ile Gly Asp Val Asn Ser Arg 625 630 635 640 Arg Gly Gln Ile Ala Ser Met Asp Asp Arg Ala Gly Ala Lys Leu Val 645 650 Lys Ala Lys Val Pro Leu Ser Gln Met Phe Gly Tyr Val Gly Asp Leu 660 665 670 Arg Ser Lys Thr Gln Gly Arg Ala Asn Tyr Ser Met Val Phe Asp Ser 680 685 Tyr Ala Glu Val Pro Ala Asn Val Ala Asp Val Ile Ala Glu Arg 690 695 700 Asn Gly Thr Ala Ser 705 <210> 3 <211> 948 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(925) <223> RXA01913 <400> 3 acctgtacga tcacttttta gacgggcggg tagggctact gtgccctaac ctaagcttgt 60

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925

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Pro Val Thr Val Ser Ala Thr Pro Met Asp Glu Pro Ala Asn Ser Ile 165 170 175

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624

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295

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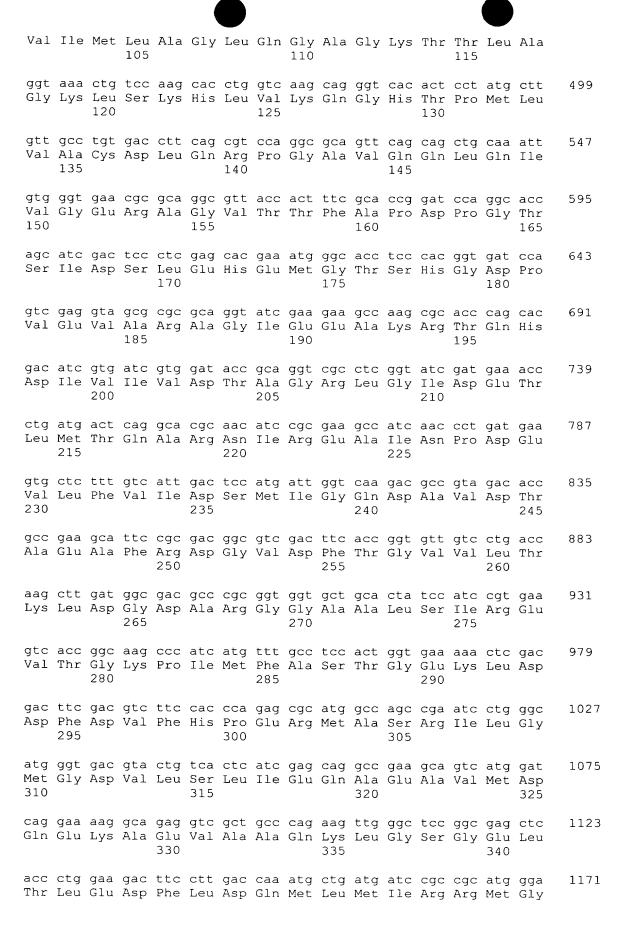
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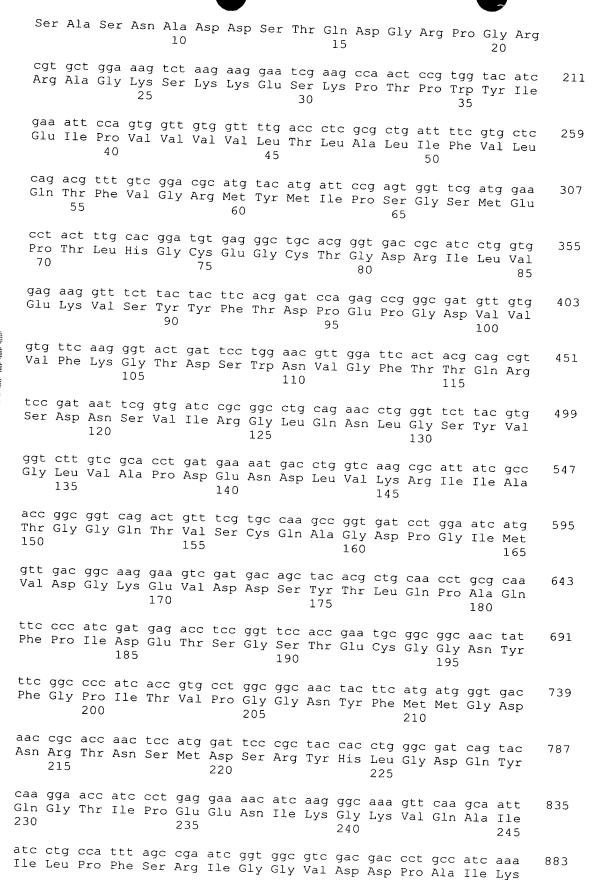
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- Ser Gln Ala Leu Asn Pro Ala Gln Gln Val Ile Lys Ile Val Asn Glu 65 70 75 80
- Glu Leu Val Gln Ile Leu Gly Gly Glu Thr Arg Arg Leu Ser Leu Ala 85 90 95
- Lys Asn Pro Pro Thr Val Ile Met Leu Ala Gly Leu Gln Gly Ala Gly 100 105 110
- Lys Thr Thr Leu Ala Gly Lys Leu Ser Lys His Leu Val Lys Gln Gly 115 120 125
- His Thr Pro Met Leu Val Ala Cys Asp Leu Gln Arg Pro Gly Ala Val 130 135 140
- Gln Gln Leu Gln Ile Val Gly Glu Arg Ala Gly Val Thr Thr Phe Ala 145 150 155 160
- Pro Asp Pro Gly Thr Ser Ile Asp Ser Leu Glu His Glu Met Gly Thr 165 170 175
- Ser His Gly Asp Pro Val Glu Val Ala Arg Ala Gly Ile Glu Glu Ala 180 185 190
- Lys Arg Thr Gln His Asp Ile Val Ile Val Asp Thr Ala Gly Arg Leu 195 200 205
- Gly Ile Asp Glu Thr Leu Met Thr Gln Ala Arg Asn Ile Arg Glu Ala 210 215 220
- Ile Asn Pro Asp Glu Val Leu Phe Val Ile Asp Ser Met Ile Gly Gln 235 230 235
- Asp Ala Val Asp Thr Ala Glu Ala Phe Arg Asp Gly Val Asp Phe Thr 245 250 255
- Gly Val Val Leu Thr Lys Leu Asp Gly Asp Ala Arg Gly Gly Ala Ala 260 265 270
- Leu Ser Ile Arg Glu Val Thr Gly Lys Pro Ile Met Phe Ala Ser Thr 275 280 285
- Gly Glu Lys Leu Asp Asp Phe Asp Val Phe His Pro Glu Arg Met Ala 290 295 300
- Ser Arg Ile Leu Gly Met Gly Asp Val Leu Ser Leu Ile Glu Gln Ala 305 310 315 320
- Glu Ala Val Met Asp Gln Glu Lys Ala Glu Val Ala Ala Gln Lys Leu 325 330 335

Gly Ser Gly Glu Leu Thr Leu Glu Asp Phe Leu Asp Gln Met Leu Met Ile Arg Arg Met Gly Pro Ile Gly Asn Ile Leu Lys Met Leu Pro Gly Gly Lys Gln Met Ser Gln Met Ala Asp Met Val Asp Glu Lys Gln Leu 375 Asp Arg Ile Gln Ala Ile Ile Arg Gly Met Thr Pro Ala Glu Arg Asp Asn Pro Lys Ile Leu Asn Ala Ser Arg Arg Lys Arg Ile Ala Asn Gly 405 410 Ser Gly Val Thr Val Ser Glu Val Asn Lys Leu Val Glu Arg Phe Phe Glu Ala Arg Lys Met Met Gly Gln Met Ala Gly Gln Phe Gly Met Gly Pro Gly Ser Arg Ser Ala Thr Lys Lys Gln Ala Lys Gly Arg Lys Gly Lys Asn Gly Lys Arg Lys Pro Ala Lys Lys Gly Pro Thr Gln Pro Lys Met Pro Met Gly Gly Met Pro Gly Met Pro Gly Met Gly Gly Ala Gly Met Pro Asp Leu Ala Glu Leu Gln Lys Gln Leu Gly Gly 505 Ala Gly Gly Met Gly Gly Leu Gly Gly Leu Pro Gly Met Pro 525 Lys Pro Pro Lys Gly Met Glu Asn Ile Asp Leu Asn Asn Leu Asp Phe 535 540 Gly Lys Lys 545 <210> 17 <211> 909 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(886) <223> RXA01355 <400> 17 aggcgcatgg cgccgaggtg cagctttggg cgaagaagta tttttcggca cacgtgtgat 60 tcaggtcagc cttaatgtaa tgctgctaga gtgaactccc gtg act gat ttt tct 115 Val Thr Asp Phe Ser agt gct tca aat gct gac gat tcc acg cag gac ggt cgt cct ggt cga 163



250 255

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Leu Ile Phe Val Leu Gln Thr Phe Val Gly Arg Met Tyr Met Ile Pro 50 60

Ser Gly Ser Met Glu Pro Thr Leu His Gly Cys Glu Gly Cys Thr Gly 65 70 75 80

Asp Arg Ile Leu Val Glu Lys Val Ser Tyr Tyr Phe Thr Asp Pro Glu 85 90 95

Pro Gly Asp Val Val Phe Lys Gly Thr Asp Ser Trp Asn Val Gly 100 105 110

Phe Thr Thr Gln Arg Ser Asp Asn Ser Val Ile Arg Gly Leu Gln Asn 115 120 125

Leu Gly Ser Tyr Val Gly Leu Val Ala Pro Asp Glu Asn Asp Leu Val 130 135 140

Lys Arg Ile Ile Ala Thr Gly Gly Gln Thr Val Ser Cys Gln Ala Gly 145 150 155 160

Asp Pro Gly Ile Met Val Asp Gly Lys Glu Val Asp Asp Ser Tyr Thr 165 170 175

Leu Gln Pro Ala Gln Phe Pro Ile Asp Glu Thr Ser Gly Ser Thr Glu 180 185 190

Cys Gly Gly Asn Tyr Phe Gly Pro Ile Thr Val Pro Gly Gly Asn Tyr 195 200 205

Phe Met Met Gly Asp Asn Arg Thr Asn Ser Met Asp Ser Arg Tyr His 210 215 220

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Asn Pro Leu Ala Ala Glu Val Ile Ala Lys Ile Glu Ala Leu Ala 65 70 75

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											atg	tct Ser	gag	cag	cca Pro 5	11
gct Ala	tcc Ser	att Ile	aag Lys	cat His 10	Tyr	gac Asp	ctc Leu	atc Ile	atc Ile 15	att Ile	ggt Gly	acc Thr	ggc Gly	tct Ser 20	gga Gly	16
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ggc Gly 390	Trp	gcc Ala	atg Met	gaa Glu	gat Asp 395	Lys	gat Asp	gga Gly	ttc Phe	gtt Val 400	Lys	ctc Leu	aat Asn	tgc Cys	cga Arg 405	1315

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Thr Gly Arg Thr Pro Asn Gly Asn Gln Met Asn Leu Asp Ala Ala Gly

285

280

Ile Glu Met Asn Gly Arg Ser Ile Lys Val Asp Glu Phe Gly Arg Thr Ser Val Glu Gly Val Trp Ala Leu Gly Asp Val Ser Ser Pro Tyr Lys 315 Leu Lys His Val Ala Asn Ala Glu Met Arg Ala Ile Lys His Asn Leu 330 Ala Asn Pro Asn Asp Leu Gln Lys Met Pro His Asp Phe Val Pro Ser 345 Ala Val Phe Thr Asn Pro Gln Ile Ser Gln Val Gly Met Thr Glu Gln 360 Glu Ala Arg Glu Ala Gly Leu Asp Ile Thr Val Lys Ile Gln Asn Tyr 375 Ser Asp Val Ala Tyr Gly Trp Ala Met Glu Asp Lys Asp Gly Phe Val Lys Leu Asn Cys Arg 405 <210> 23 <211> 600 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(577) <223> RXA00539 <400> 23 cgacctggca gttcaccttt ggtctcacca aagttcacct attagctgac ctttatttag 60 atgatgcact aaatcctccc cctcaactag ggttgcgatt atg act tct att cat 115 Met Thr Ser Ile His gac atc agc gta act ctc aac gac ggc aca gaa acc acc atg gcg gat 163 Asp Ile Ser Val Thr Leu Asn Asp Gly Thr Glu Thr Thr Met Ala Asp 10 20 tgg gcg ggc cac ctt ttg ctc atc gtg aac gtg gca tcc aag tgc gga 211 Trp Ala Gly His Leu Leu Ile Val Asn Val Ala Ser Lys Cys Gly 25 35 ctc acg cca cag tat gaa ggg ctt caa aaa ctg tat gag gaa tac caa 259 Leu Thr Pro Gln Tyr Glu Gly Leu Gln Lys Leu Tyr Glu Glu Tyr Gln 40 gat cga ggc ttc ttt gtc att ggc gtg ccc tgc aat caa ttc aac ggc 307 Asp Arg Gly Phe Phe Val Ile Gly Val Pro Cys Asn Gln Phe Asn Gly 55 cag gaa cct gga acc gac gct gag gtg tgt gct ttc gcg caa aat cag 355

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gtg Val 150	gaa Glu	gca Ala	atc Ile	gag Glu	gag Glu 155	aat Asn	ctc Leu	cct Pro	atc Ile	taaq	gggct	egg (	ctage	gttt	ga	597
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Gly	'Va	l P	he 35	Leu	Ala	Glu	Glu	Glu 40	ı Ph	ne I	Leu	Pro	Pro	Va:		sp.	Asp	V	al		
Phe	Ar 5	g A 0	la	Phe	Ser	Tyr	Pro 55	Phe	e As	p F	Ala	Val	Lys 60	: Va]	. Le	eu	Ile	Me	et		
Gly 65	Gl	n A	sp	Pro	Tyr	Pro 70	Thr	Pro	Gl	уE	lis	Ala 75	Met	Gly	' Le	u :	Ser		ne 30		
Ser	Th	r G	ln	Pro	Asp 85	Val	Arg	Pro	Le	u P	ro 90	Arg	Ser	Leu	As	n A	Asn 95	IJ	le		
Phe	Lys	s G	lu :	Leu 100	Val	Ser	Asp	Val	Gl 10	y S 5	er	Leu	Gly	Asp	Se		Ala	Se	er		
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Gln	Ala	Gl	у S	Ser	His 165	Lys	Gly	Lys	Gly	/ Ti	rp (	Glu	Ala	Val	Thi		lu 75	Gl	n		

Ala Ile Lys Ala Leu Ala Glu Arg Asp Gln Pro Leu Val Ala Ile Leu 185 Trp Gly Lys Gln Ala Gln Glu Val Gln Lys Phe Leu Gly Asp Thr Pro 200 Cys Ile Cys Ser Val His Pro Ser Pro Leu Ser Ala Ser Arg Gly Phe 215 Phe Gly Ser Lys Pro Phe Ser Arg Ala Asn Glu Ile Leu Ser Ser Leu 235 Gly Ala Thr Glu Ile Asp Trp Ser Leu 245 <210> 27 <211> 1203 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1180) <223> RXN00484 <400> 27 acgtaccggt aatccgcttg aaatactgcc gaaaatagtc tctgagatgg aagtcaaagc 60 cgtcacatgg aatcgacgct atcatcaacc gttatgtgaa gtg gat gcc act ctc 115 Val Asp Ala Thr Leu 1 aaa aag aat ctc cgt gat aaa ggg att gaa gtg cat agc cac cca ggt 163 Lys Lys Asn Leu Arg Asp Lys Gly Ile Glu Val His Ser His Pro Gly 10 20 ttt tta ctc act gaa ccc tgg gaa gtc agt acc gct acc gga act ccc 211 Phe Leu Leu Thr Glu Pro Trp Glu Val Ser Thr Ala Thr Gly Thr Pro 25 35 tac aag gta ttt acc cct ttt tct aaa gcc gca tgg gaa gta gcc aga 259 Tyr Lys Val Phe Thr Pro Phe Ser Lys Ala Ala Trp Glu Val Ala Arg 40 50 gta cat gca tat gaa act gtt aaa aac aat gtg cct gtc ccc tct cac 307 Val His Ala Tyr Glu Thr Val Lys Asn Asn Val Pro Val Pro Ser His 55 60 cta aca gga cca gag gat gta gag ctg ccc atc cta gaa atg gag caa 355 Leu Thr Gly Pro Glu Asp Val Glu Leu Pro Ile Leu Glu Met Glu Gln 70 75 cct ttt tgg tca aca acg tta gtt aag gag tgt gct ccc ggt gaa aaa 403 Pro Phe Trp Ser Thr Thr Leu Val Lys Glu Cys Ala Pro Gly Glu Lys aat gct tcg gaa aaa ctc ttt gat ttt ttg gaa cat cta cag gac tac 451 Asn Ala Ser Glu Lys Leu Phe Asp Phe Leu Glu His Leu Gln Asp Tyr 105 110

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-	cat His 135							_			_			_		547
	gca Ala	-		_		-								-		595
	tgg Trp	_	_					_			_	_			_	643
-	acg Thr			_		_										691
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	aaa Lys				_	_	-	-	_		_	-	-			835
	acc Thr															883
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	gaa Glu			_	_	_	-		-			_				979
	tgg Trp 295															1027
	aat Asn															1075
	cgt Arg	_		-		-							_	_		1123
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1203

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Ala Thr Gly Thr Pro Tyr Lys Val Phe Thr Pro Phe Ser Lys Ala Ala 35 40 45

Trp Glu Val Ala Arg Val His Ala Tyr Glu Thr Val Lys Asn Asn Val 50 55 60

Pro Val Pro Ser His Leu Thr Gly Pro Glu Asp Val Glu Leu Pro Ile 65 70 75 80

Leu Glu Met Glu Gln Pro Phe Trp Ser Thr Thr Leu Val Lys Glu Cys
85 90 95

Ala Pro Gly Glu Lys Asn Ala Ser Glu Lys Leu Phe Asp Phe Leu Glu 100 105 110

His Leu Gln Asp Tyr Pro Gln Ala Arg Asp Ser Leu Ala Arg Ser Ala 115 120 125

Thr Ser Lys Leu Ser Ala His Leu Arg Phe Gly Glu Ile Ser Ile His 130 135 140

Arg Val Trp Ala Glu Thr Ala Ala Ile Asp Ser Glu Gly Thr Glu Leu 145 150 155 160

Phe Leu Lys Glu Leu Trp Arg Asp Phe Ala Trp His Arg Leu Tyr
165 170 175

Ala Leu Pro His Met Asp Thr Gln Asn Val Arg Met Gln Phe Asn Arg 180 185 190

Phe Gly Trp Ser Trp Asp Pro Ser Glu Lys Asp Lys Leu Asn Thr Pro 195 200 205

Ser Thr Pro Leu Ile Pro Thr Lys Ala Asp Gln Phe His Glu Asp Leu 210 215 220

Ala Ala Trp Arg Ala Gly Lys Thr Gly Ile Pro Leu Val Asp Ala Gly 225 230 235 240

Met Arg Glu Leu Trp Ala Thr Gly Ser Met His Asn Arg Val Arg Met 245 250 255

Val Val Ala Ser Phe Leu Thr Lys Asn Leu Gln Ile His Trp Arg His 260 265 270

Gly Glu Glu Trp Phe Trp Glu Thr Leu Val Asp Ala Asp Pro Ala Ser Asn Ala Phe Asn Trp Gln Trp Ala Ala Gly Ser Gly Asp Asp Ala Ser Pro Tyr Phe Arg Ile Phe Asn Pro Val Thr Gln Ala Lys Lys Phe Asp Pro Asp Glu Thr Tyr Ile Arg Arg Trp Val Pro Glu Tyr Gly Thr Pro 330 Ser Tyr Pro Asp Pro Ile Val Asp Leu Lys Glu Ser Arg Gln Ile Ala 340 345 Leu Asp Ala Tyr Ser Ala Ile Lys 355 <210> 29 <211> 1158 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1135) <223> FRXA00484 <400> 29 gatggaagtc aaagccgtca catggaatcg acgctatcat caaccgttat gtgaagtgga 60 tgccactctc aaaaagaatc tccgtgataa agggattgaa gtg cat agc cac cca 115 Val His Ser His Pro ggt ttt tta ctc act gaa ccc tgg gaa gtc agt acc gct acc gga act 163 Gly Phe Leu Leu Thr Glu Pro Trp Glu Val Ser Thr Ala Thr Gly Thr 10 ccc tac aag gta ttt acc cct ttt tct aaa gcc gca tgg gaa gta gcc 211 Pro Tyr Lys Val Phe Thr Pro Phe Ser Lys Ala Ala Trp Glu Val Ala aga gta cat gca tat gaa act gtt aaa aac aat gtg cct gtc ccc tct 259 Arg Val His Ala Tyr Glu Thr Val Lys Asn Asn Val Pro Val Pro Ser cac cta aca gga cca gag gat gta gag ctg ccc atc cta gaa atg gag 307 His Leu Thr Gly Pro Glu Asp Val Glu Leu Pro Ile Leu Glu Met Glu caa cct ttt tgg tca aca acg tta gtt aag gag tgt gct ccc ggt gaa 355 Gln Pro Phe Trp Ser Thr Thr Leu Val Lys Glu Cys Ala Pro Gly Glu 75 aaa aat gct tcg gaa aaa ctc ttt gat ttt ttg gaa cat cta cag gac 403 Lys Asn Ala Ser Glu Lys Leu Phe Asp Phe Leu Glu His Leu Gln Asp 95 100

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gca Ala	gga Gly 215	aaa Lys	aca Thr	gga Gly	att Ile	ccg Pro 220	ctg Leu	gtc Val	gat Asp	gca Ala	ggc Gly 225	atg Met	cga Arg	gaa Glu	tta Leu	787
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				aat Asn 250												883
				ctc Leu												931
				gcg Ala											cgt Arg	979
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ccc Pro	atc Ile	gtc Val	gat Asp	ctg Leu 330	aaa Lys	gaa Glu	tcc Ser	cgt Arg	caa Gln 335	Ile	gct Ala	tta Leu	gac Asp	gcc Ala 340	tac Tyr	1123
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Ala Trp Glu Val Ala Arg Val His Ala Tyr Glu Thr Val Lys Asn Asn 35 40 45

Val Pro Val Pro Ser His Leu Thr Gly Pro Glu Asp Val Glu Leu Pro 50 55 60

Ile Leu Glu Met Glu Gln Pro Phe Trp Ser Thr Thr Leu Val Lys Glu 65 70 75 80

Cys Ala Pro Gly Glu Lys Asn Ala Ser Glu Lys Leu Phe Asp Phe Leu 85 90 95

Glu His Leu Gln Asp Tyr Pro Gln Ala Arg Asp Ser Leu Ala Arg Ser 100 105 110

Ala Thr Ser Lys Leu Ser Ala His Leu Arg Phe Gly Glu Ile Ser Ile 115 120 125

His Arg Val Trp Ala Glu Thr Ala Ala Ile Asp Ser Glu Gly Thr Glu 130 135 140

Leu Phe Leu Lys Glu Leu Leu Trp Arg Asp Phe Ala Trp His Arg Leu 145 150 155 160

Tyr Ala Leu Pro His Met Asp Thr Gln Asn Val Arg Met Gln Phe Asn 165 170 175

Arg Phe Gly Trp Ser Trp Asp Pro Ser Glu Lys Asp Lys Leu Asn Thr 180 185 190

Pro Ser Thr Pro Leu Ile Pro Thr Lys Ala Asp Gln Phe His Glu Asp 195 200 205

Leu Ala Ala Trp Arg Ala Gly Lys Thr Gly Ile Pro Leu Val Asp Ala 210 215 220

Gly Met Arg Glu Leu Trp Ala Thr Gly Ser Met His Asn Arg Val Arg 225 230 235 240

Met Val Val Ala Ser Phe Leu Thr Lys Asn Leu Gln Ile His Trp Arg 245 250 255

His Gly Glu Glu Trp Phe Trp Glu Thr Leu Val Asp Ala Asp Pro Ala 260 265 270

Ser Asn Ala Phe Asn Trp Gln Trp Ala Ala Gly Ser Gly Asp Asp Ala 280 Ser Pro Tyr Phe Arg Ile Phe Asn Pro Val Thr Gln Ala Lys Lys Phe 295 Asp Pro Asp Glu Thr Tyr Ile Arg Arg Trp Val Pro Glu Tyr Gly Thr 315 Pro Ser Tyr Pro Asp Pro Ile Val Asp Leu Lys Glu Ser Arg Gln Ile Ala Leu Asp Ala Tyr Ser Ala Ile Lys 340 <210> 31 <211> 1002 -<212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(979) <223> RXA02476 <400> 31 cgggcggagt tctatcaaca ttacgcaaag gcataagctt tattattcca ctcggtgtga 60 catatgacct aaagtgccag tcagtacaat catttaggtc atg tca ttt aca gct Met Ser Phe Thr Ala ttt caa aca gcc ctg ctc gtg tgg ttt aga gca aat gcc cgc gat ctt 163 Phe Gln Thr Ala Leu Leu Val Trp Phe Arg Ala Asn Ala Arg Asp Leu gcg tgg cgt gat ccc aat act tca gca tgg gga att ctc ctt tca gag 211 Ala Trp Arg Asp Pro Asn Thr Ser Ala Trp Gly Ile Leu Leu Ser Glu 30 gtg atg agc caa caa act ccc gtc gcg cga gtc gag ccg att tgg cgt 259 Val Met Ser Gln Gln Thr Pro Val Ala Arg Val Glu Pro Ile Trp Arg gag tgg atg gaa aaa tgg ccc act ccg gaa gat ttc gcg aat gcg agc 307 Glu Trp Met Glu Lys Trp Pro Thr Pro Glu Asp Phe Ala Asn Ala Ser acc gat gag att ttg cgg tcg tgg ggc aag ttg ggc tat cca cgt agg 355 Thr Asp Glu Ile Leu Arg Ser Trp Gly Lys Leu Gly Tyr Pro Arg Arg gcg ctg agg ttg aag gaa tgt gcg gag gtg atc gtc gaa aag cat gcc 403 Ala Leu Arg Leu Lys Glu Cys Ala Glu Val Ile Val Glu Lys His Ala ggc gag gtg ccg gat acg gtg gag gcg ctg ctc gcg ttg ccg ggg atc Gly Glu Val Pro Asp Thr Val Glu Ala Leu Leu Ala Leu Pro Gly Ile 105 110

115

ggt gat tac Gly Asp Tyr 120	Thr Ala								499
gtg ccg gtg Val Pro Val 135		-	Val Arg		-			-	547
gcc gga cgt Ala Gly Arg 150					/s Gln			-	595
gtc tcc ctt Val Ser Leu		Pro Asn		-	_		_	-	643
ata atg gag Ile Met Glu		-	_				Lys	-	691
gac acc tgc Asp Thr Cys 200	Pro Leu	-		_				-	739
ccc tcc ccg Pro Ser Pro 215				_	-			_	787
aaa ttt gtg Lys Phe Val 230			_		y Leu	-	-	-	835
ctg cgc aat Leu Arg Asn	-	Ala Pro				-	_		883
tgg cct gac Trp Pro Asp		-		Ala Le	_	_	Ile		931
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Ile Leu Leu Ser Glu Val Met Ser Gln Gln Thr Pro Val Ala Arg Val 35  $\phantom{\bigg|}40\phantom{\bigg|}$ 

Glu Pro Ile Trp Arg Glu Trp Met Glu Lys Trp Pro Thr Pro Glu Asp 50 55 60

Phe Ala Asn Ala Ser Thr Asp Glu Ile Leu Arg Ser Trp Gly Lys Leu 65 70 75 80

Gly Tyr Pro Arg Arg Ala Leu Arg Leu Lys Glu Cys Ala Glu Val Ile 85 90 95

Val Glu Lys His Ala Gly Glu Val Pro Asp Thr Val Glu Ala Leu Leu 100 105 110

Ala Leu Pro Gly Ile Gly Asp Tyr Thr Ala Arg Ala Val Ala Ala Phe 115 120 125

His Phe Gly Gln Arg Val Pro Val Val Asp Thr Asn Val Arg Arg Val 130 135 140

Tyr Gln Arg Ala Val Ala Gly Arg Tyr Leu Ala Gly Pro Ala Lys Lys 145 150 155 160

Gln Glu Leu Ile Asp Val Ser Leu Leu Leu Pro Asn Thr His Ala Pro 165 170 175

Glu Phe Ser Ala Ala Ile Met Glu Leu Gly Ala Leu Ile Cys Thr Ala 180 185 190

Thr Ser Pro Lys Cys Asp Thr Cys Pro Leu Leu Asp Gln Cys Gln Trp 195 200 205

Gln Lys Leu Gly Cys Pro Ser Pro Ser Glu Glu Glu Leu Ala Ser Ala 210 215 220

Lys Lys Arg Val Gln Lys Phe Val Gly Thr Asp Arg Gln Val Arg Gly 225 235 240

Leu Ile Met Asp Val Leu Arg Asn Ala Thr Ala Pro Val Pro Leu Ser 245 250 255

Ala Ile Asp Val Val Trp Pro Asp Asp Ala Gln Arg Ser Arg Ala Leu 260 265 270

Phe Ser Leu Ile Glu Asp Gly Leu Ala Glu Gln Asn Glu Ala Gly Tyr 275 280 285

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891

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240

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Val	Ile	His	Arg	Leu	Ala	Gly	Glu	Leu	Thr	Lys	Asn	Phe	ĞÎv	Ásp	Thr	
				10					15				-	20		

att	ttg	gac	gcc	act	tca	cct	caa	gga	cqc	ttt	act	tct	gaa	aca	aca	211
Ile	Leu	Asp	Ala	Thr	Ser	Pro	Gln	Ğĺy	Arq	Phe	Thr	Ser	Glu	Ala	Ala	211
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Ile	Ile	Asn	Gly	His	Arq	Ile	Ala	Val	Ala	Glu	Ala	Tyr	Glv	Luc	Hie	239
		40			,		45					50	Ory	цуз	111.3	

ctg	ttc	gtc	gag	ttc	gat	qcq	gat	cac	cct	gag	cac	att	tta	tat	atc	307
Leu	Phe	Val	Glu	Phe	Āsn	Δla	Δen	Hie	Dro	Clu	1110	T1-	T	m	-1	307
	55				1100	60	1100	1113	110	Gru		тте	ьeu	ryr	TIE	
						00					65					

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uls	ьeu	$ar\lambda$	Leu	TTe	GLy	Thr	Leu	Gln	Phe	Glu	Pro	Ala	Glu	Glu	Thr	
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Arg	ggg	Gln	Ile	Arg	Leu	His	Leu	Ser	Asp	Gly	Glu	Ile	Ala	Ala	Asn	
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Leu	Arg	Gly	Pro	Gln	Trp	Cys	Arg	Leu	Ile	Thr	Asp	Ala	Glu	Ara	Thr	431
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		120					125					130				

ccg Pro	GIU	cca Pro	att Ile	cgg Arg	att Ile	Lys	gtg Val	cag Gln	cgc Arg	tca Ser	Gly ggg	cga Arg	agc Ser	att Ile	ggt Gly	547
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cgt Arg	geo g Ala	g gag n Glu	aca Thr	ctt Leu 170	Phe	cgc Arg	ctg Leu	Gly	att Ile 175	Ser	ccg Pro	ttc Phe	acc Thr	att Ile 180	gga Gly	643
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Pro	Ala	Glu	Glu	Thr . 85	Arg (	Gly	Gln	Ile A	Arg :	Leu	His	Leu	Ser	Asp	Gly	

Glu Ile Ala Ala Asn Leu Arg Gly Pro Gln Trp Cys Arg Leu Ile Thr 100 105 110

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95

90

403

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Ala Ala Arg Asn Gln Leu Gly Gly Gly Pro Glu Ile Glu Ala Asn Ile  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

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Leu Leu Val His Leu Gly Met Ser Gly Gln Met Leu Ile Lys Glu Pro 85 90 95

Asp Ala Pro Ile Ser Pro His Leu Arg Ala Lys Val Glu Leu Asp Asn 100 105 110

Gly Asp Glu Val Trp Phe Val Asp Gln Arg Thr Phe Gly Tyr Trp Trp 115 120 125

Leu Gly Asp Leu Val Asp Gly Val Pro Glu Arg Val Ser His Ile Ala 130 135 140

Thr Asp Val Leu Asp Glu Ser Ala Asp Phe Ser Ala Ile Ala Arg Asn 145 150 155 160

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Ile Val Ser Gly Ile Gly Asn Ile Tyr Ala Asp Glu Met Leu Trp Gln
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Ala Lys Ile His Pro Leu Gln Arg Ala Asp Arg Leu Ser Leu Ala Arg 195 200 205

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LCu	V CL I	1135	1114	110	CL	шуз	11011	110	ritg	AL 9	Val	Val	TILL	$O = \lambda$	пси	
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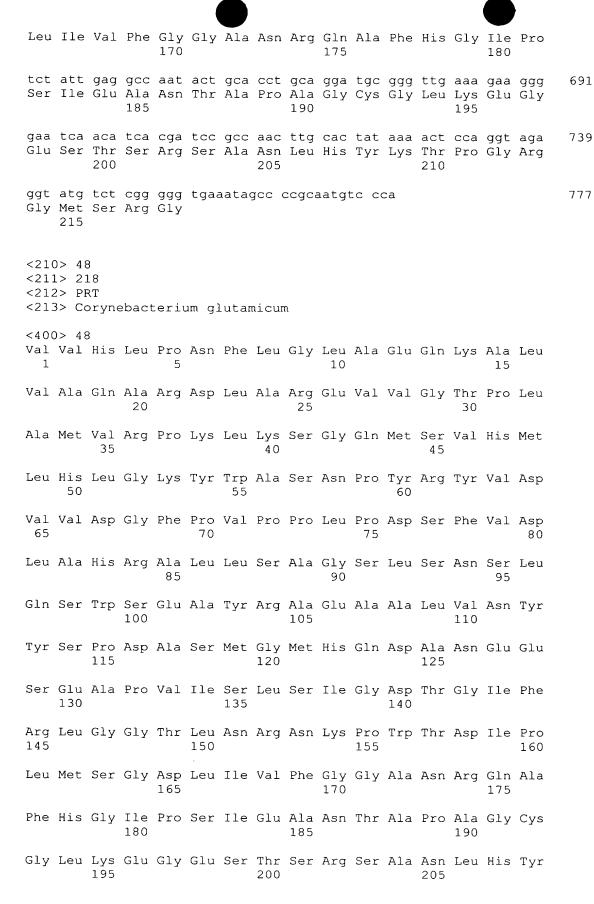
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691

739

777

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cga gaa ttg gca gct cac ttg ctg atc aaa ccc cat gct gcg aat cag 351 Arg Glu Leu Ala Ala His Leu Leu Ile Lys Pro His Ala Ala Asn Gln 85 80

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Gly Phe Gly Lys Thr Asn Ile Val Glu Ala Ile Gly Tyr Leu Ala His  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Leu Ser Ser His Arg Val Ser Ser Asp Ala Pro Leu Val Arg Ala His 50 55 60

Ala Glu Asn Ala Arg Val Ser Ala Val Ala Val Asn Gln Gly Arg Glu 65 70 75 80

Leu Ala Ala His Leu Leu Ile Lys Pro His Ala Ala Asn Gln Ala Ser 85 90 95

Leu Asn Arg Thr Lys Val Arg Thr Pro Arg Glu Leu Leu Gly Val Val 100 105 110

Lys Thr Val Leu Phe Ala Pro Glu Asp Leu Ala Leu Val Lys Gly Glu 115 120 125

Pro Ala Glu Arg Arg Tyr Leu Asp Asp Ile Ile Ala Thr Arg Gln 130 135 140

Pro Arg Met Ala Gly Val Lys Ala Asp Tyr Asp Lys Val Leu Lys Gln 145 150 155 160

Arg Asn Ala Leu Leu Lys Thr Ala Thr Ile Ala Leu Arg Arg Gly Tyr
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Gly Thr Glu Glu Gly Ala Ala Ala Leu Ser Thr Leu Asp Thr Trp Asp 180 185 190

Gly Gln Leu Ala Arg Leu Gly Ala Glu Val Met Ala Ala Arg Phe Ala 195 200 205

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Ala Pro Glu Ser Arg Pro Ala Ala Val Asn Tyr Lys Thr Thr Ile Asp 225 230 235 240

Gln Gly Leu Ser Gln Phe Ser Glu Phe Asp Ala Gly Ile Ile Glu Ala 245 250 255

Thr Leu Leu Thr Glu Leu Ala Ala Lys Arg Gln Arg Glu Ile Glu Arg 260 265 270

Gly Ser Ser Leu Val Gly Pro His Arg Asp Asp Val Asp Leu Met Leu 275 280 285

Gly Asp Gln Pro Ala Lys Gly Phe Ala Ser His Gly Glu Thr Trp Ser 290 295 300

Ph 30	e Ala 5	a Le	u Se	r Le	a Arc 310	g Il∈	e Ala	a Glu	ı Phe	e Asr 315		ı Leı	ı Lys	s Sei	r Asp 320	
Gl	y Thi	r As <sub>l</sub>	p Pr	o Ile 325	e Leu	ı Ile	e Lei	ı Asp	Asp 330		l Ph∈	e Ser	Glı	Let 335	ı Asp	
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Lys	370	. Lei	ı Thı	Ala	Gln	His 375	Thr	Val	Thr	· Val	Gln 380		Thr	Gly	Thr	
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cga Arg	att Ile	gca Ala	gaa Glu 100	ttt Phe	aac Asn	ctg Leu	ctg Leu	aaa Lys 105	tcc Ser	gat Asp	ggc Gly	acc Thr	gac Asp 110	ccg Pro	atc Ile	336
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gca gtc cac ga Ala Val His As 145	c gat ctg ccg p Asp Leu Pro 150	g gag aat cto Glu Asn Leu	c aag aaa gtg c 1 Lys Lys Val Le 155	cc act gcg 480 eu Thr Ala 160
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Leu Ala Ala Lys 50	Arg Gln Arg 55	Glu Ile Glu	Arg Gly Ser Se	r Leu Val
Gly Pro His Arg 65	Asp Asp Val 70	Asp Leu Met	Leu Gly Asp Gl	n Pro Ala . 80
Lys Gly Phe Ala	Ser His Gly 85		Ser Phe Ala Le	
Arg Ile Ala Glu 100	Phe Asn Leu	Leu Lys Ser 105	Asp Gly Thr As	_
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Lys Leu Val Gly 130	Ile Ala Gln 135	Glu Val Glu	Gln Val Leu Il 140	e Thr Ala
Ala Val His Asp 145	Asp Leu Pro 150	Glu Asn Leu	Lys Lys Val Le 155	u Thr Ala 160
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691

739

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Arg	Ile 130	Gly	Gly	Val	Leu	Pro 135	Asp	Arg	Glu	Leu	Ala 140	Asp	Ser	Thr	Pro
Glu 145	Asn	Lys	Leu	Phe	Asp 150	Ala	Thr	Pro	Thr	Val 155	Arg	Glu	Val	Ile	Leu 160
Ala	Thr	Asp	Pro	Asn 165	Thr	Glu	Gly	Glu	Ala 170	Thr	Ala	Ser	Tyr	Leu 175	Gly
Arg	Leu	Leu	Lys 180	Asp	Phe	Pro	Asp	Leu 185	Val	Ile	Ser	Arg	Leu 190	Ala	Ser
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125

120

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aaa

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His Leu Gly His Val Trp Asn Asp Arg Leu Thr Phe Glu Tyr Ser Arg 20 25 30

Ser Leu Phe Gly Lys Glu Thr Leu Ser Pro Asp Ile Ala Arg Leu Phe 35 40 45

Thr Asp Arg Val Pro Thr Pro Pro Leu Pro Ala Pro Arg Lys Ala Arg 50 55 60

Ala Val Ala Gln Val Leu Val Ser Asn Pro Ala Asp Gln Thr Ser Leu 65 70 75 80

Glu Glu Phe Ala Glu Ile Gln Gly Val Ser Ala Arg Thr Leu Gln Arg 85 90 95

Gln Phe Leu Lys Ser Thr Gly Tyr Ser Phe Ser Glu Trp Arg Ala Ala 100 105 110

Gln Arg Val Cys Val Ala Ala Ser Leu Leu Ala His Asp Phe Ser Ile 115 120 125

Ser Val Val Ala Asn Leu Val Gly Phe Ala Ala Thr Ser Ser Leu Thr 130 135 140

Arg Ala Phe Arg Arg His Thr Gly Ala Thr Pro Ser Thr Phe Thr Thr 145 150 155 160

Gly Gln Ile Gly Met Gly Ser Ala Gly His Pro Pro Arg Ile Pro Ala 165 170 175

Thr Thr Thr Phe Ala Glu Ala His Gln Asp Gln Gln Leu Trp Ile Tyr 180 185 190

Ser Gly Thr Ala Thr Val Thr Thr Pro Gly Tyr Cys Arg Phe Met Gly 195 200 205

Gln Gly Asp Met Val Thr Ile Pro Ala Gly Thr Gln Thr Arg Ile Asp 210 215 220

Val Ala Ala Gly Ser Ile Ala Phe Pro Val Pro Val Gly Leu Asp Glu 225 230 235 240

Trp Gly Met Asp Leu Thr Arg Val Val Ala Val Asn Asn Gln Gln Pro  $245 \hspace{1cm} 250 \hspace{1cm} 255$ 

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                                             Val Lys Lys Arg Ile
aat gta acc ggc gcc gtc cta gtc aag gaa aac cgt atc ctt gca gca
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Gln Arg Gly Pro Glu Met Ser Leu Pro Gly Tyr Trp Glu Phe Pro Gly
gga aag atc gag cag ggc gaa act cca gaa gct tca ctt gca cga gag
                                                                    259
Gly Lys Ile Glu Gln Gly Glu Thr Pro Glu Ala Ser Leu Ala Arg Glu
ctc aaa gaa gaa ttg ctt tgc gac gcc acc gta ggc gaa cac ctc acc
                                                                    307
Leu Lys Glu Glu Leu Leu Cys Asp Ala Thr Val Gly Glu His Leu Thr
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act aca gag cac gag tac gac ttt gga atc gtc gtg ctt tcc acc tac
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Thr Thr Glu His Glu Tyr Asp Phe Gly Ile Val Val Leu Ser Thr Tyr
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                                                                    403
Phe Cys Thr Leu Asn Asp Ala Glu Pro Gln Leu Thr Glu His Ala Glu
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Ile Arg Trp Val Ala Pro His Glu Leu Glu Ser Leu Glu Trp Ala Pro
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                                 110
gct gat att cct gcg gtg aaa ctt ctc gtc gag cag ctt gct
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					gtc Val											403
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				_	acc Thr		_			_		_	_			499
_				_	gat Asp		_		_	_		_	_	_	_	547
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Gly Asp Thr Trp Ala Leu Pro Gly Gly Ala Arg Asp Ser His Glu Thr

Ala Ala Glu Ser Ala Leu Arg Glu Ala Phe Glu Glu Thr Gly Ile Leu

Pro Asp Asp Val Glu Val Leu Asp Ser Ile Val Thr Ala Gly Pro Phe 85

Pro Ala Asp Pro Glu Arg Pro Glu Leu Ala Gly Asn Trp Thr Tyr Thr 105

Thr Val Ile Ala Arg Thr Lys Thr Gly Glu Thr Leu Asp Thr Thr Ala 115

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gee eee tte Ala Pro Phe	gtt ccg Val Pro 25	cgc acc	c cgc Arg	gaa Glu 30	cca Pro	cat His	tta Leu	aat Asn	aaa Lys 35	tgg Trp	gca Ala	211
ctg ccc ggc Leu Pro Gly 40	GLY Trp	ctg cca Leu Pro	cca Pro 45	cat His	gaa Glu	gaa Glu	ctt Leu	gaa Glu 50	gat Asp	gct Ala	gct Ala	259
gcc cgc aca Ala Arg Thr 55	ctc gca Leu Ala	gaa acc Glu Thr 60	Thr	ggc Gly	ctg Leu	cac His	ccc Pro 65	agc Ser	tat Tyr	cta Leu	gaa Glu	307
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gcc atc cca Ala Ile Pro	gga gaa Gly Glu 105	aac gtc Asn Val	Gln	tgg Trp 110	ttt Phe	ccc Pro	gcc Ala	gat Asp	cat His 115	ctc Leu	cct Pro	451
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ctt cgc acc Leu Arg Thr 135	aag gtg Lys Val	gaa tac Glu Tyr 140	tcc (	gaa Glu	atc Ile	Ala	cac His 145	tcc Ser	ttc Phe	ctc Leu	gga Gly	547
gaa acc ttc Glu Thr Phe 150	int ife	gcc cag Ala Gln 155	ctt d Leu A	cga : Arg :	Ser	gtg Val 160	cat His	gag Glu	gca Ala	gtc Val	ctt Leu 165	595
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ccc gat ctg Pro Asp Leu	atc gac Ile Asp 185	acc ggc Thr Gly	Glu V	gtg d /al I 190	ctt ( Leu /	gcg ( Ala (	gga a Gly :	Thr	ccg Pro 195	cac His	cgc Arg	691
cca ccc aaa Pro Pro Lys 200	ctg ttc . Leu Phe ?	aga ttc Arg Phe	caa a Gln A 205	nga t Arg	caaat	ttctq	ga co	gctc	attc	С		738
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Leu Glu Asp Ala Ala Ala Arg Thr Leu Ala Glu Thr Thr Gly Leu His

Pro Ser Tyr Leu Glu Gln Leu Tyr Thr Phe Gly Lys Val Asp Arg Ser

Pro Thr Gly Arg Val Ile Ser Val Val Tyr Trp Ala Leu Val Arg Ala

Asp Glu Ala Leu Lys Ala Ile Pro Gly Glu Asn Val Gln Trp Phe Pro 100 105

Ala Asp His Leu Pro Glu Leu Ala Phe Asp His Asn Asn Ile Val Lys 115 120

Tyr Ala Leu Glu Arg Leu Arg Thr Lys Val Glu Tyr Ser Glu Ile Ala 130

His Ser Phe Leu Gly Glu Thr Phe Thr Ile Ala Gln Leu Arg Ser Val

His Glu Ala Val Leu Gly His Lys Leu Asp Ala Ala Asn Phe Arg Arg 165

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cca cag ccg gag acc ctg gag gag att ccg acg cag tcg ccg gag tca

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ccc Pro	acg Thr	acg Thr	atg Met	ttt Phe 170	gcc Ala	ctt Leu	atg Met	gaa Glu	gcc Ala 175	ata Ile	gga Gly	atc Ile	gtc Val	gac Asp 180	acc Thr	643
cat His	ttg Leu	gtg Val	ggc Gly 185	agc Ser	cat His	cgc Arg	cgc Arg	gga Gly 190	agt Ser	tct Ser	ggg Gly	gtg Val	tgg Trp 195	gct Ala		688
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Ala Phe Gln Ser Gly Leu Ser Trp Ala Thr Ile Leu Arg Lys Arg Asp

Ser Phe Arg Ala Ala Phe Ser Gln Phe Asp Pro Glu Leu Val Ala Lys 75

Phe Thr Asp Ala Asp Ile Glu Arg Leu Met Glu Asp Ala Gly Ile Val

Arg Asn Lys Arg Lys Ile Leu Ala Thr Ile Asn Asn Ala Lys Ala Thr 105

Leu Gln Leu Arg Glu Lys Gly Gly Leu Val Glu Phe Val Trp Gly Phe 120

Lys Pro Ile Asp Thr Pro Gln Pro Glu Thr Leu Glu Glu Ile Pro Thr

Gln Ser Pro Glu Ser Val Ala Leu Ser Lys Ala Leu Lys Lys Glu Gly

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                                                          15
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                                            Met Ser Glu Gln Arg
ctc gat cag ctt gag cga cgg ctt tct gaa ctg gaa cgg gag atc gcc
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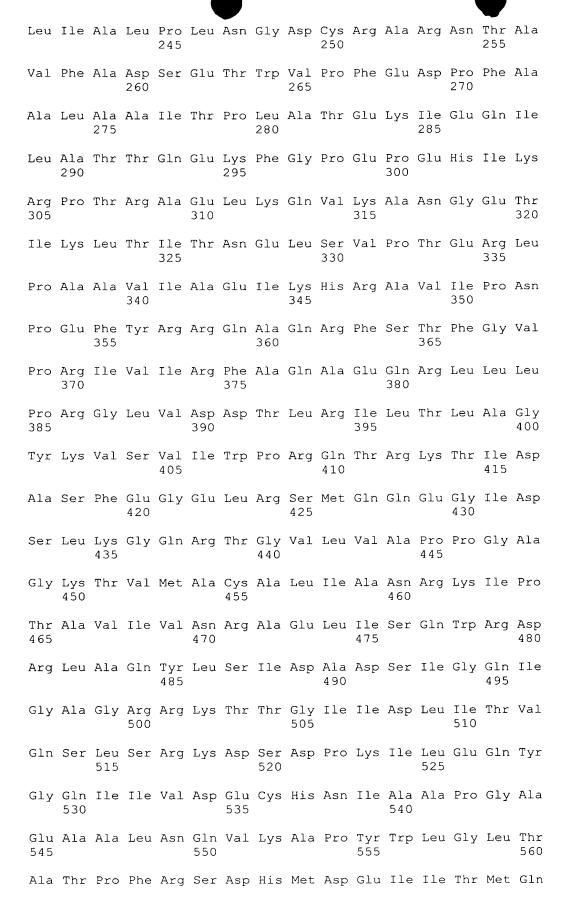
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BGI-127CP - 100 -



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gat Asp	gtc Val	gat Asp 280	gaa Glu	gtc Val	gga Gly	ctc Leu	gat Asp 285	cgc Arg	ctg Leu	gat Asp	agg Arg	gca Ala 290	gtg Val	ctt Leu	gat Asp	979
gcc Ala	ttg Leu 295	atc Ile	cgc Arg	gga Gly	cat His	ggc Gly 300	gga Gly	ggc Gly	cct Pro	gtt Val	ggc Gly 305	gtg Val	aac Asn	aca Thr	ctc Leu	1027
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ccc Pro	tat Tyr	ttg Leu	gtg Val	cgt Arg 330	gcc Ala	ggc Gly	atg Met	Ile	gca Ala 335	cga Arg	acc Thr	gga Gly	cgg Arg	gga Gly 340	cgc Arg	1123
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<213> Corynebacterium glutamicum

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Ala Asn Leu Lys Pro Asp Glu Tyr Asp Ala Glu Val Thr Leu Arg Pro
35 40 45

Lys Ser Leu Thr Glu Phe Ile Gly Gln Pro Lys Val Arg Asp Gln Leu 50 60

Ser Leu Val Leu Thr Gly Ala Lys Asn Arg Gly Val Val Pro Asp His 65 70 75 80

Val Leu Leu Ser Gly Pro Pro Gly Leu Gly Lys Thr Thr Met Ala Met 85 90 95

Ile Ile Ala Gln Glu Leu Gly Thr Ser Leu Arg Met Thr Ser Gly Pro
100 105 110

Ala Leu Glu Arg Ala Gly Asp Leu Ala Ala Met Leu Ser Asn Leu Met 115 120 125

Glu Gly Asp Val Leu Phe Ile Asp Glu Ile His Arg Ile Ala Arg Pro 130 135 140

Ala Glu Glu Met Leu Tyr Met Ala Met Glu Asp Phe Arg Ile Asp Val 145 150 155 160

Ile Val Gly Lys Gly Pro Gly Ala Thr Ser Ile Pro Leu Glu Ile Pro 165 170 175

Pro Phe Thr Leu Val Gly Ala Thr Thr Arg Ser Gly Met Leu Thr Gly 180 185 190

Pro Leu Arg Asp Arg Phe Gly Phe Thr Ala Gln Met Glu Phe Tyr Asp 195 200 205

Val Pro Asp Leu Thr Lys Val Val Lys Arg Thr Ala Lys Ile Leu Asp 210 215 220

Val Gly Ile Asp Asn Asp Ala Ala Val Glu Ile Ala Ser Arg Ser Arg 225 230 235 240

Gly Thr Pro Arg Ile Ala Asn Arg Leu Leu Arg Arg Val Arg Asp Phe 245 250 255

Ala Glu Val His Ala Asp Gly His Ile Thr Met Gly Ala Ala Asn Ala 260 265 270

Ala Leu Ile Val Phe Asp Val Asp Glu Val Gly Leu Asp Arg Leu Asp 275 280 285

Arg Ala Val Leu Asp Ala Leu Ile Arg Gly His Gly Gly Pro Val

290

295 300

Gly Val Asn Thr Leu Ala Val Ala Val Gly Glu Glu Pro Gly Thr Val 305 310 315 320

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<222> (101)..(718)

<223> RXA00928

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cgt ggc act gtt atc aac att ggt ctg agc tct gct gtc att gaa tgc 163 Arg Gly Thr Val Ile Asn Ile Gly Leu Ser Ser Ala Val Ile Glu Cys 10 15 20

aat ggc gtg ggc tat gag gtt gtc acc aca ccg aac acc ttg tca cag 211 Asn Gly Val Gly Tyr Glu Val Val Thr Thr Pro Asn Thr Leu Ser Gln

ttg gtc cgc ggt gag gaa gca ctg gtg ttg acc acc atg gtg gtc cgc 259 Leu Val Arg Gly Glu Glu Ala Leu Val Leu Thr Thr Met Val Val Arg

gaa gac gcg atg aaa ctc tat ggg ttt att gac aat gaa tca cgt gag 307 Glu Asp Ala Met Lys Leu Tyr Gly Phe Ile Asp Asn Glu Ser Arg Glu 55 60 65

atg ttt tcc gtg ttg caa aca gta tct gga ttg ggt cca cgc ctg gcc 355

Met Phe Ser Val Leu Gln Thr Val Ser Gly Leu Gly Pro Arg Leu Ala
70 80 85

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Leu Ala Cys Glu Ser Val Leu Ser Pro Leu Glu Ile Ser Gln Ala Ile
90 95 100

acc aat gcc gat gcc aaa act ttg cag cgg gtt ccg ggt gtg gga aag 451
Thr Asn Ala Asp Ala Lys Thr Leu Gln Arg Val Pro Gly Val Gly Lys
105 110 115

cgc atg gca gat cgt ctc atc gtg gag ctt aaa ggc aag gtc gca gct 499

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gcc Ala	gca Ala	ttg Leu 200	gca Ala	aaa Lys	ctc Leu	agc Ser	gga Gly 205	aag Lys	taga	accct	ca t	gtco	cgato	gt		738
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Gln Val Ser Gln Ala Leu Val Gly Leu Gly Phe Ser Glu Lys Gln Ser 165 170 Asp Asp Ala Val Ser Phe Val Leu Ala Ala Asp Pro Ser Leu Asp Thr

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ttt aag gaa caa aca act aac ccg aga agt caa cga gtt tct tat ttg 163 Phe Lys Glu Gln Thr Thr Asn Pro Arg Ser Gln Arg Val Ser Tyr Leu 10 20

cgt gtc tct agc acc gat cag aat ctg gct cga caa cgt gaa gct gtt 211 Arg Val Ser Ser Thr Asp Gln Asn Leu Ala Arg Gln Arg Glu Ala Val 25

aac cat too ggt cat att gat cgt gag tto aca gat gag ctt too ggt 259 Asn His Ser Gly His Ile Asp Arg Glu Phe Thr Asp Glu Leu Ser Gly 40 45

ggc gcc aaa tca cac aga cct ggc ttg gaa gac tgc att aat tat ctt 307 Gly Ala Lys Ser His Arg Pro Gly Leu Glu Asp Cys Ile Asn Tyr Leu 55 60

cgc gag gat gat gtt ctt gtc gtc gca tcc att gac cga ctt gca cgc 355 Arg Glu Asp Asp Val Leu Val Val Ala Ser Ile Asp Arg Leu Ala Arg 70 75

tcg ctg gtt gat tta cgc gtc atc att gac cgc atc aca gac aaa ggc 403 Ser Leu Val Asp Leu Arg Val Ile Ile Asp Arg Ile Thr Asp Lys Gly 90

gca tcg gtc att ttt ctc aaa gag aat ttg act ttc gct gca ggc cgc 451 Ala Ser Val Ile Phe Leu Lys Glu Asn Leu Thr Phe Ala Ala Gly Arg 105

gat gat cct cga gca aac ctc atg ctc ggt att ttg ggc agt ttc gca 499 Asp Asp Pro Arg Ala Asn Leu Met Leu Gly Ile Leu Gly Ser Phe Ala 120 125

gaa ttt gaa cgc tca att att cgc gag cgc caa gca gaa ggt att gcc 547

595

643

691

735

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Arg	Val	Ser	Tyr 20	Leu	Arg	Val	Ser	Ser 25	Thr	Asp	Gln	Asn	Leu 30	Ala	Arg
Gln	Arg	Glu 35	Ala	Val	Asn	His	Ser 40	Gly	His	Ile	Asp	Arg 45	Glu	Phe	Thr
Asp	Glu 50	Leu	Ser	Gly	Gly	Ala 55	Lys	Ser	His	Arg	Pro 60	Gly	Leu	Glu	Asp
Cys 65	Ile	Asn	Tyr	Leu	Arg 70	Glu	Asp	Asp	Val	Leu 75	Val	Val	Ala	Ser	Ile 80
Asp	Arg	Leu	Ala	Arg 85	Ser	Leu	Val	Asp	Leu 90	Arg	Val	Ile	Ile	Asp 95	Arg
Ile	Thr	Asp	Lys 100	Gly	Ala	Ser	Val	Ile 105	Phe	Leu	Lys	Glu	Asn 110	Leu	Thr
Phe	Ala	Ala 115	Gly	Arg	Asp	Asp	Pro 120	Arg	Ala	Asn	Leu	Met 125	Leu	Gly	Ile
Leu	Gly 130	Ser	Phe	Ala	Glu	Phe 135	Glu	Arg	Ser	Ile	Ile 140	Arg	Glu	Arg	Gln
Ala 145	Glu	Gly	Ile	Ala	Leu 150	Ala	Lys	Lys	Ala	Gly 155	Lys	Tyr	Ala	Gly	Arg 160
Pro	Lys	Ala	Leu	Asp 165	Lys	Glu	Gln	Ile	Gln 170	Glu	Ala	Lys	Asp	Met 175	Ile
Ala	Gln	Gly	Glu 180	Thr	Lys	Ser	Ala	Val 185	Ala	Lys	His	Phe	Gly 190	Ile	Asn

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ggc gcc aaa tca cac aga cct Gly Ala Lys Ser His Arg Pro 55 60	ggc ttg gaa gac Gly Leu Glu Asp	tgc att aat tat Cys Ile Asn Tyr 65	ctt 307 Leu
cgc gag gat gat gtt ctt gtc Arg Glu Asp Asp Val Leu Val 70 75	gtc gca tcc att Val Ala Ser Ile 80	gac cga ctt gca Asp Arg Leu Ala	cgc 355 Arg 85
tcg ctg gtt gat tta cgc gtc Ser Leu Val Asp Leu Arg Val 90	atc att gac cgc Ile Ile Asp Arg 95	atc aca gac aaa Ile Thr Asp Lys 100	ggc 403 Gly
gca tcg gtc att ttt ctc aaa a Ala Ser Val Ile Phe Leu Lys ( 105	gag aat ttg act Glu Asn Leu Thr 110	ttc gct gca ggc Phe Ala Ala Gly 115	cgc 451 Arg

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gaa Glu	ttt Phe 135	gaa Glu	cgc Arg	tca Ser	att Ile	att Ile 140	cgc Arg	gag Glu	cgc Arg	caa Gln	gca Ala 145	gaa Glu	ggt Gly	att Ile	gcc Ala	547
ctg																550

550

Leu .

150

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Asp Leu Gln Ile Gly Met Thr Arg Trp Phe Leu Ser Asp Glu Ala Gln gcc cgt ttt gac gat gac cgg att agg gcc atc gaa aag atg ggc aag 259 Ala Arg Phe Asp Asp Asp Arg Ile Arg Ala Ile Glu Lys Met Gly Lys 45 ate gea egg aaa aat eag tge gag tte att gtg ete gee gge gae gte 307 Ile Ala Arg Lys Asn Gln Cys Glu Phe Ile Val Leu Ala Gly Asp Val ttc gag cac aac tct tta gaa caa cgc acc act gga cgt gcc tta gaa 355 Phe Glu His Asn Ser Leu Glu Gln Arg Thr Thr Gly Arg Ala Leu Glu gcc tta cga tcc tta aag ctg ccg gtt tat ctg ctg ccg ggt aac cat 403 Ala Leu Arg Ser Leu Lys Leu Pro Val Tyr Leu Leu Pro Gly Asn His gat cct tta aca gcg gat tcg ttg ttt tac cgc gcc aaa gat att gat Asp Pro Leu Thr Ala Asp Ser Leu Phe Tyr Arg Ala Lys Asp Ile Asp 110 ggc gtg aca atc ttg tcg gac acc acc gtg cat ggg gtg gcc cct ggg 499 Gly Val Thr Ile Leu Ser Asp Thr Thr Val His Gly Val Ala Pro Gly 125 gtg gaa att att gga gca ccc ttg ctg cac aag atg gct act tca gat 547 Val Glu Ile Ile Gly Ala Pro Leu Leu His Lys Met Ala Thr Ser Asp 140 cta gtg gca gaa gca ttg aaa gat ttg gaa cca acc tcc aac gtc cgt 595 Leu Val Ala Glu Ala Leu Lys Asp Leu Glu Pro Thr Ser Asn Val Arg 160 atc gct gtg ggg cac ggc caa gca gaa gct cgc acc act gac cac cgg 643 Ile Ala Val Gly His Gly Gln Ala Glu Ala Arg Thr Thr Asp His Arg 170 gct gac tta atc gat ctg aac act gtt gaa gcc aaa ttg gct gac ggt 691 Ala Asp Leu Ile Asp Leu Asn Thr Val Glu Ala Lys Leu Ala Asp Gly 190 acg att gac tac ctc gct ctc ggc gat acc cac tcg gct cag cca gta 739 Thr Ile Asp Tyr Leu Ala Leu Gly Asp Thr His Ser Ala Gln Pro Val ggt acc agt gga aaa gtc tgg ttt tct gga gct cca gag acc aca gac 787 Gly Thr Ser Gly Lys Val Trp Phe Ser Gly Ala Pro Glu Thr Thr Asp 220 ttc cat gac tta gat cca gac cgt gtg ggc ggt gag gtg aac tct ggc 835 Phe His Asp Leu Asp Pro Asp Arg Val Gly Gly Glu Val Asn Ser Gly 235 240 aaa gtt ctc att gtc agc gcc tca aag ggt gac gtt tca gtc gaa gaa 883 Lys Val Leu Ile Val Ser Ala Ser Lys Gly Asp Val Ser Val Glu Glu 255 gtc gag gtg ggg aag tgg acc ttc cac gct tta tct aaa gaa atc acc 931 Val Glu Val Gly Lys Trp Thr Phe His Ala Leu Ser Lys Glu Ile Thr

265 270 275 tcg ggt acc gat gtg gaa gat ttc ttg gat acc ttg cag gca tac cct 979 Ser Gly Thr Asp Val Glu Asp Phe Leu Asp Thr Leu Gln Ala Tyr Pro 285 gat aaa tot oga aca gto ato aaa tat ggt oto ogo gga aco ato aco 1027 Asp Lys Ser Arg Thr Val Ile Lys Tyr Gly Leu Arg Gly Thr Ile Thr 300 ctg gaa caa aac agg cgt ttg gaa gaa ggc atc gct ggg tta gaa gat 1075 Leu Glu Gln Asn Arg Arg Leu Glu Glu Gly Ile Ala Gly Leu Glu Asp 310 315 320 gto tit got toa oto aag oot ogg gaa ogo aco act gao oto gtg otg 1123 Val Phe Ala Ser Leu Lys Pro Arg Glu Arg Thr Thr Asp Leu Val Leu 330 gag cca ggg gag gaa gaa tta gcc aat ctc gat gcc aca ggt tac gcc 1171 Glu Pro Gly Glu Glu Leu Ala Asn Leu Asp Ala Thr Gly Tyr Ala 350 gct gaa gta ttg cga gag ctc gct gac tct gtg gtc aat ggt gca gcg 1219 Ala Glu Val Leu Arg Glu Leu Ala Asp Ser Val Val Asn Gly Ala Ala 365 ccg gaa gaa gac cgc gat gcg ctc aac cta ttg ttc cga cta agc cgg 1267 Pro Glu Glu Asp Arg Asp Ala Leu Asn Leu Leu Phe Arg Leu Ser Arg 385 gag gtc taagacatgc gtattcatga aat 1296 Glu Val 390 <210> 88 <211> 391 <212> PRT <213> Corynebacterium glutamicum <400> 88 Met Ser Thr Val His Asp Glu Met Gly Val Met Asn Thr Thr Val Lys Phe Leu His Ser Ser Asp Leu Gln Ile Gly Met Thr Arg Trp Phe Leu Ser Asp Glu Ala Gln Ala Arg Phe Asp Asp Asp Arg Ile Arg Ala Ile Glu Lys Met Gly Lys Ile Ala Arg Lys Asn Gln Cys Glu Phe Ile Val Leu Ala Gly Asp Val Phe Glu His Asn Ser Leu Glu Gln Arg Thr Thr 65 75 Gly Arg Ala Leu Glu Ala Leu Arg Ser Leu Lys Leu Pro Val Tyr Leu 90 Leu Pro Gly Asn His Asp Pro Leu Thr Ala Asp Ser Leu Phe Tyr Arg 100 105

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Gly Val Ala Pro Gly Val Glu Ile Ile Gly Ala Pro Leu Leu His Lys 130 135 140

Met Ala Thr Ser Asp Leu Val Ala Glu Ala Leu Lys Asp Leu Glu Pro 145 150 155 160

Thr Ser Asn Val Arg Ile Ala Val Gly His Gly Gln Ala Glu Ala Arg 165 170 175

Thr Thr Asp His Arg Ala Asp Leu Ile Asp Leu Asn Thr Val Glu Ala 180 185 190

Lys Leu Ala Asp Gly Thr Ile Asp Tyr Leu Ala Leu Gly Asp Thr His 195 200 205

Ser Ala Gln Pro Val Gly Thr Ser Gly Lys Val Trp Phe Ser Gly Ala 210 215 220

Pro Glu Thr Thr Asp Phe His Asp Leu Asp Pro Asp Arg Val Gly Gly 235 230 235

Glu Val Asn Ser Gly Lys Val Leu Ile Val Ser Ala Ser Lys Gly Asp 245 250 255

Val Ser Val Glu Glu Val Glu Val Gly Lys Trp Thr Phe His Ala Leu 260 265 270

Ser Lys Glu Ile Thr Ser Gly Thr Asp Val Glu Asp Phe Leu Asp Thr 275 280 285

Leu Gln Ala Tyr Pro Asp Lys Ser Arg Thr Val Ile Lys Tyr Gly Leu 290 295 300

Arg Gly Thr Ile Thr Leu Glu Gln Asn Arg Arg Leu Glu Glu Gly Ile 305 310 315 320

Ala Gly Leu Glu Asp Val Phe Ala Ser Leu Lys Pro Arg Glu Arg Thr 325 330 335

Thr Asp Leu Val Leu Glu Pro Gly Glu Glu Glu Leu Ala Asn Leu Asp 340 345 350

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Phe Arg Leu Ser Arg Glu Val 385 390

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<211> 1983

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gac aag att atc gac att aat ttg ttg gct gtt ttc tca ggc att ggt

739

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Asp	Lys	Ile 200	Ile	Asp	Ile	Asn	Leu 205	Leu	Ala	Val	Phe	Ser 210	Gly	Ile	Gly	
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	cag Gln															835
	cgt Arg															883
	acg Thr															931
	ttc Phe		_	_										_	_	979
	gcg Ala 295		_	_		-			_							1027
	ggc Gly															1075
	gac Asp															1123
	tca Ser															1171
	att Ile															1219
	gcc Ala 375															1267
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Arg Ala Thr Ala Leu Ile His Asp His Ile Thr Lys Ala Gln Glu Ile 50 55 60

Thr Ile Ile Thr Asp Phe Asp Met Asp Gly Ile Ser Ala Gly Val Ile 65 70 75 80

Ala Tyr Ala Gly Leu Ala Glu Leu Gly Ala Gln Val Asn Met Val Val 85 90 95

Pro Asp Tyr Arg Gly Glu Arg Asn Val Thr Ala Ser Asp Ile Asp Arg 100 105 110

Ala Leu Glu Leu Tyr Pro Ala Thr Ser Leu Ile Ile Thr Cys Asp Val 115 120 125

Gly Ile Gly Ser His Glu Gly Ile Ala Arg Ala His Glu Arg Ser Ile 130 135 140

Ala Val Leu Val Thr Asp His His Met Glu Val Glu Pro Cys Gln Ala 145 150 155 160

Asp Val Val Leu Asn Pro Asn Arg Ile Asp Ser Asp Tyr Pro Asn Lys 165 170 175

Asp Ile Cys Gly Ala Gln Val Ile Phe Ala Thr Leu Ser Asp Tyr Ala 180 185 190

Arg Arg Tyr Arg Ala Asp Lys Ile Ile Asp Ile Asn Leu Leu Ala Val 195 200 205

Phe Ser Gly Ile Gly Ala Leu Ala Asp Val Met Pro Leu Thr Arg Asp 210 215 220

Thr Arg Pro Thr Val Lys Gln Ala Ile Ala Leu Leu Arg Leu Ala Ile 225 230 235 240

Pro Gln Val Ser Lys Asn Arg Phe Gly Gly Trp Asp Thr Tyr Ala Ala 245 250 255

Arg Ser Val Asn Pro Asp Thr Ser Thr Leu Met His Ile Val Asn Ala 260 265 270

Ser Gln His Asp His Arg Phe Ile Ala Ala Phe Gln Gly Ile Ser Ile 275 280 285

Leu Leu Gly Glu Leu Ile Ala Gln Lys Lys Leu Val Asn Ile Asp Asn 290 295 300

Ile Ser Glu Ser Phe Ile Gly Phe Thr Leu Gly Pro Met Phe Asn Ala 305 310 315 320

Thr Arg Arg Val Gly Gly Asp Met His Asp Ser Phe Leu Val Phe Ala 325 330 335

Pro His Ala Ala Leu Ala Ser Gln Pro Ser Met Asn Pro Asn Arg His 340 345 350

Ala Ala Ile Ser Arg Ile Ile Asp Asn Asn Glu Arg Arg Lys Glu Leu 355 360 365

Ser Lys Ser Ser Tyr Ala Ala Val His Ser Ser Asp Gln Pro Tyr Ala 370 375 380

Ala Ser Gln Leu Thr Arg Glu Ser Asp Val Pro Ala Ile Val Ile Asn 405 410 415

Pro Asp Thr Leu Ser Gly Ser Ala Arg Ser Pro Glu Trp Ala Pro Ile 420 425 430

Ile Thr Gln Val Asn Thr Leu Ser Ala Gln Gly His Gly Gly Ile His 435 440 445

Ala Ala Gly His Glu Tyr Ala Cys Gly Met Arg Phe Asp Asn His Asp 450 455 460

Asp Ile Val Thr Phe Val Ala Thr Leu Asp Ala Leu Asp Lys Asn Thr 465 470 475 480

Pro Arg Glu Ala Gln Pro Ala Asp Leu His Leu Val Asp Ile Asp His 485 490 495

Ala Arg Pro Val Leu Asp Asn Pro Ser Leu Thr Gln Glu Leu Ser Thr 500 505 510

Val Asp Ala Ala Val Asp Ala Ala Gln Leu Leu Val Leu Ile Asp Gln 515 520 525

Leu Asp Gln Leu Gln Pro Phe Gly His Gly Phe Thr Tyr Pro Arg Ile 530 535 540

Asp Val Thr Phe Arg Pro Ala Glu Thr Glu Phe Lys Val Met Gly Gln 545 550 560

His His Gln His Leu Lys Val Ile Thr His Ser Gly Leu Thr Leu Leu 565 570 575

Trp Trp Asn Lys Ala Gln Gln Leu Asp Glu Ile Ala Gln Ser Glu Leu 580 585 590

Val Thr Met Ser Val Glu Leu Asp Val Asn Met Phe Arg Gly Phe Ile 595 600 605

Ser Pro Gln Gly Ile Val Ser Ala Cys Thr Val Ile 610 615 620

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<222> (101)..(763)

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ctt Leu	cgg Arg	gta Val	atg Met	ggc Gly 10	att	gac Asp	cca Pro	ggt Gly	ctt Leu 15	acc Thr	cgt Arg	tgt Cys	ggc Gly	tta Leu 20	tct Ser	163
gtg Val	gtt Val	caa Gln	gca Ala 25	Gly	cgt Arg	ggt Gly	cgt Arg	acc Thr 30	gtg Val	tat Tyr	cca Pro	gtg Val	tcg Ser 35	gtg Val	ggc Gly	211
gtg Val	gtg Val	cgc Arg 40	acc Thr	cca Pro	cca Pro	gat Asp	gcg Ala 45	gag Glu	ttg Leu	gcg Ala	gag Glu	cgg Arg 50	ttg Leu	ctt Leu	cgg Arg	259
ctc Leu	agc Ser 55	aaa Lys	gca Ala	gtg Val	ggt Gly	gag Glu 60	tgg Trp	atg Met	gat Asp	gag Glu	tac Tyr 65	acc Thr	cca Pro	gat Asp	gtc Val	307
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gga Gly	ttg Leu	cca Pro	gtt Val 105	cac His	atg Met	tac Tyr	acc Thr	ccc Pro 110	agt Ser	gag Glu	gtg Val	aaa Lys	aag Lys 115	gct Ala	atc Ile	451
tcc Ser	ggt Gly	aat Asn 120	ggt Gly	cgc Arg	gct Ala	gat Asp	aag Lys 125	aaa Lys	cag Gln	atg Met	acg Thr	gtc Val 130	atg Met	atc Ile	act Thr	499
cga Arg	att Ile 135	ctg Leu	ggc Gly	ctt Leu	ggt Gly	gag Glu 140	cca Pro	ccc Pro	aaa Lys	cct Pro	gct Ala 145	gac Asp	gcc Ala	gct Ala	gat Asp	547
gct Ala 150	tta Leu	tcg Ser	ttg Leu	gcg Ala	gtg Val 155	tgt Cys	cac His	tgc Cys	tgg Trp	cgg Arg 160	gcg Ala	cca Pro	atg Met	ctt Leu	atg Met 165	595
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gtg Val	cag Gln	caa Gln	gga Gly 185	aaa Lys	ttg Leu	ggt Gly	aaa Lys	gcg Ala 190	aaa Lys	tca Ser	act Thr	tac Tyr	aat Asn 195	gcg Ala	gaa Glu	691
caa Gln	gct Ala	caa Gln 200	tcc Ser	cat His	gca Ala	tcc Ser	gat Asp 205	cct Pro	gct Ala	aaa Lys	gcg Ala	gct Ala 210	cat His	ccc Pro	agt Ser	739
cag Gln	ttt Phe 215	caa Gln	cga Arg	act Thr	gac Asp	acc Thr 220	aat Asn	tagt	tttt	aa a	ıaagt	tcta	ıg ta	.C		786

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<212> PRT

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<400> 92

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20 25 30

Pro Val Ser Val Gly Val Val Arg Thr Pro Pro Asp Ala Glu Leu Ala 35 40 45

Glu Arg Leu Leu Arg Leu Ser Lys Ala Val Gly Glu Trp Met Asp Glu 50 55 60

Tyr Thr Pro Asp Val Ile Ala Ile Glu Arg Val Phe Glu Arg Gly Asn 65 70 75 80

Val Ser Thr Val Met Asn Thr Ala His Ala Val Gly Val Leu Ile Leu 85 90 95

Ala Ala Ala Glu Arg Gly Leu Pro Val His Met Tyr Thr Pro Ser Glu 100 105 110

Val Lys Lys Ala Ile Ser Gly Asn Gly Arg Ala Asp Lys Lys Gln Met 115 120 125

Thr Val Met Ile Thr Arg Ile Leu Gly Leu Gly Glu Pro Pro Lys Pro 130 135 140

Ala Asp Ala Ala Asp Ala Leu Ser Leu Ala Val Cys His Cys Trp Arg 145 150 155 160

Ala Pro Met Leu Met Arg Ala Gln Ser Gln Tyr Ser Glu Gln Glu Leu 165 170 175

Glu Lys Arg Arg Val Gln Gln Gly Lys Leu Gly Lys Ala Lys Ser 180 185 190

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aaa Lys	ttc Phe	agg Arg	gac Asp 25	gaa Glu	aac Asn	cgc Arg	cgc Arg	gtg Val 30	atc Ile	tac Tyr	gtg Val	ggc Gly	aag Lys 35	gcc Ala	aaa Lys	211
aac Asn	ttg Leu	cgt Arg 40	tcg Ser	cgg Arg	ttg Leu	tcg Ser	aac Asn 45	tat Tyr	ttc Phe	cag Gln	gat Asp	gtc Val 50	acc Thr	caa Gln	ctg Leu	259
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acc Thr 70	gtg Val	gtg Val	tcc Ser	agc Ser	gaa Glu 75	gtc Val	gag Glu	gcg Ala	ctg Leu	cag Gln 80	ctg Leu	gaa Glu	tac Tyr	acc Thr	tgg Trp 85	355
att Ile	aaa Lys	cgc Arg	ttt Phe	gat Asp 90	ccg Pro	cgg Arg	ttc Phe	aaa Lys	cgt Arg 95	aaa Lys	ata Ile	ccg Pro	cga Arg	cga Arg 100		400
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Glu	Pro	Gly	Val 20	Tyr	Lys	Phe	Arg	Asp 25	Glu	Asn	Arg	Arg	Val 30	Ile	Tyr	
Val	Gly	Lys 35	Ala	Lys	Asn	Leu	Arg 40	Ser	Arg	Leu	Ser	Asn 45	Tyr	Phe	Gln	
Asp	Val 50	Thr	Gln	Leu	His	Pro 55	Arg	Thr	Arg	Gln	Met 60	Val	Phe	Ala	Ala	
Ser 65	Ser	Val	Glu	Trp	Thr 70	Val	Val	Ser	Ser	Glu 75	Val	Glu	Ala	Leu	Gln 80	
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gco Ala	c gto u Val	g caa . Gln	gtc Val 185	Phe	: aac : Asn	atc Ile	cga Arg	ggt Gly 190	Gly	cga Arg	ato Ile	cgc Arg	ggc Gly 195	, Glr	g cgc n Arg	691
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345

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- 132 -

Asp Ser Met Glu Thr Ala Leu Arg Leu Ala Asp Gly Val Ala Val Leu

220

DOMONDERO LOGINOS



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Val Glu Ser Leu Ser Ser Tyr Ala Arg Met Phe Leu Gly Gln Met Asp 50 55 60

Lys Pro Asp Val Asp Leu Ile Asp Gly Leu Ser Pro Ala Val Ser Ile 65 70 75 80

Thr Glu Val Tyr Asp Tyr Leu Arg Leu Leu Tyr Ala Arg Ala Gly Thr 100 105 110

Ala His Cys Pro Val Cys Asp Ala Arg Val Glu Arg Gln Thr Pro Gln 115 120 125

Gln Met Val Asp Gln Ile Leu Gly Met Glu Glu Gly Leu Lys Phe Gln 130 135 140

Ile Leu Ala Pro Val Val Arg Thr Arg Lys Gly Glu Phe Val Asp Leu 145 150 155 160

Phe Ala Asp Leu Ala Ser Gln Gly Tyr Ser Arg Val Arg Val Asp Gly 165 170 175

Glu Val His Gln Leu Ser Asp Pro Pro Lys Leu Glu Lys Gln Ile Lys 180 185 190

His Asp Ile Asp Val Val Val Asp Arg Leu Gln Val Lys Ala Ser Gln 195 200 205

Lys Gln Arg Leu Thr Asp Ser Met Glu Thr Ala Leu Arg Leu Ala Asp 210 215 220

Gly Val Ala Val Leu Glu Phe Val Gly Leu Glu Glu Asp Asp Pro Asn 225 230 235 240

Arg Leu Arg Arg Phe Ser Glu Lys Met Ser Cys Pro Asn Gly His Ala 245 250 255

Leu Thr Val Asp Glu Leu Glu Pro Arg Ala Phe Ser Phe Asn Ser Pro 260 260 270

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576

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ctg Leu	gtt Val	gat Asp 755	gtc Val	ggc Gly	ctt Leu	ggc Gly	tat Tyr 760	gtc Val	cgt Arg	ttg Leu	ggc Gly	cag Gln 765	gca Ala	gca Ala	aca Thr	2304
acc Thr	ttg Leu 770	tct Ser	ggt <sup>°</sup> Gly	ggt Gly	gaa Glu	gcc Ala 775	cag Gln	cgt Arg	gtg Val	aaa Lys	ctt Leu 780	gcc Ala	gct Ala	gag Glu	ctg Leu	2352
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ggc (	ctg Leu	gtg Val	gac Asp 820	aag Lys	ggt Gly	aac Asn	tcc Ser	gtg Val 825	atc Ile	atc Ile	atc Ile	gag Glu	cac His 830	aac Asn	ctc Leu	2496
gac ( Asp \	vaı	atc Ile 835	aag Lys	gct Ala	gcc Ala	gac Asp	tgg Trp 840	atc Ile	gtg Val	gac Asp	atg Met	ggt Gly 845	cca Pro	gag Glu	ggc Gly	2544
gga a Gly s	agc Ser 350	ggc Gly	ggt Gly	gga Gly	Thr	gtg Val 855	gtc Val	gct Ala	gaa Glu	gga Gly	acc Thr 860	cca Pro	gag Glu	caa Gln	gtt Val	2592
gct o Ala ( 865	gaa Slu	gtt Val	gcg Ala	ggt Gly	tcc Ser 870	tac Tyr	acc Thr	ggc Gly	caa Gln	ttc Phe 875	ctt Leu	aaa Lys	gag Glu	ttg Leu	ttg Leu 880	2640
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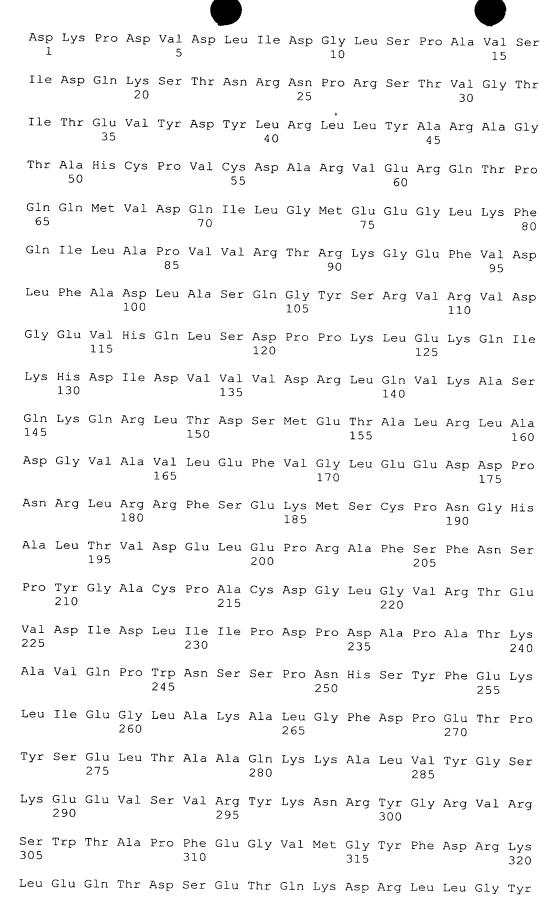
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<400> 100



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Glu Thr Thr Glu Ala Lys Val Arg Gly Tyr Lys Pro Gly Arg Phe Ser 660 665 670

Phe Asn Ile Lys Gly Gly Arg Cys Glu Ala Cys Gln Gly Asp Gly Thr 675 680 685

Leu Lys Ile Glu Met Asn Phe Leu Pro Asp Val Tyr Val Pro Cys Glu 690 695 700

Val Cys Asp Gly Gln Arg Tyr Asn Arg Glu Thr Leu Glu Val Lys Tyr 705 710 715 720

Lys Gly Lys Asn Ile Ala Glu Val Leu Gly Met Pro Ile Ser Glu Ala 725 730 735

Ala Asp Phe Phe Glu Pro Ile Thr Ser Ile His Arg Tyr Leu Ala Thr 740 745 750

Leu Val Asp Val Gly Leu Gly Tyr Val Arg Leu Gly Gln Ala Ala Thr 755 760 765

Thr Leu Ser Gly Gly Glu Ala Gln Arg Val Lys Leu Ala Ala Glu Leu 770 780

Gln Lys Arg Ser Asn Gly Arg Thr Val Tyr Ile Leu Asp Glu Pro Thr 785 790 795 800

Thr Gly Leu His Phe Glu Asp Ile Arg Lys Leu Met Met Val Ile Glu 805 810 815

Gly Leu Val Asp Lys Gly Asn Ser Val Ile Ile Ile Glu His Asn Leu 820 825 830

Asp Val Ile Lys Ala Ala Asp Trp Ile Val Asp Met Gly Pro Glu Gly 835 840 845

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Met Met Pro Tyr Ile acc gat att gca gcg ctt gaa cat gtg ggt gtg gct gct gct tgg aca 163 Thr Asp Ile Ala Ala Leu Glu His Val Gly Val Ala Ala Ala Trp Thr gag aag gtt cct gct ttt cgg gtg ttg aga gaa aag cgc atg ctg gac 211 Glu Lys Val Pro Ala Phe Arg Val Leu Arg Glu Lys Arg Met Leu Asp ttt cgt gcg ccg atc acc gtc ata acc ggg gaa aac ggt gtg ggt aag 259 Phe Arg Ala Pro Ile Thr Val Ile Thr Gly Glu Asn Gly Val Gly Lys tcg aca ttg ctg gag gct atc gcg atc aat gcg ggc ttc gac aca gca 307 Ser Thr Leu Leu Glu Ala Ile Ala Ile Asn Ala Gly Phe Asp Thr Ala 60 ggt ggt gaa cac acc gga aag ttc aaa cct tcc gac aac cct ttg caa 355 Gly Gly Glu His Thr Gly Lys Phe Lys Pro Ser Asp Asn Pro Leu Gln act gtg gca aaa gca cac aag gga aaa gag ccg atg cgg ggg tat ttc 403 Thr Val Ala Lys Ala His Lys Gly Lys Glu Pro Met Arg Gly Tyr Phe ctg cgg gcg gaa act cat ttc aac gtc gcg tct gga tat cgc gat gag 451 Leu Arg Ala Glu Thr His Phe Asn Val Ala Ser Gly Tyr Arg Asp Glu gct ccc ggc tgg gtg aac ctt cat cac atg tcg cac ggg gag tcg gtg 499 Ala Pro Gly Trp Val Asn Leu His His Met Ser His Gly Glu Ser Val 125 atg cat att gtg cag aat gct ttt gtg ggc aag ggg ctg tat ctg atg 547 Met His Ile Val Gln Asn Ala Phe Val Gly Lys Gly Leu Tyr Leu Met 140 gat gag cct gaa gcg ggg cta tcg ttc att cga cag atg gcg att ctg 595 Asp Glu Pro Glu Ala Gly Leu Ser Phe Ile Arg Gln Met Ala Ile Leu 155 gcg gag ctt aat ttt ctg gcg gaa agt ggt gcg caa att atc atc gtg 643 Ala Glu Leu Asn Phe Leu Ala Glu Ser Gly Ala Gln Ile Ile Val 170 175 acg cat tcg ccg gtg ttg atg gct att ccg ggt gca gaa att tgg gag 691 Thr His Ser Pro Val Leu Met Ala Ile Pro Gly Ala Glu Ile Trp Glu 190 ttt agt gca tcg ggg gaa ctg cat cga ggg ttt gat ttt gag gtg aca 739 Phe Ser Ala Ser Gly Glu Leu His Arg Gly Phe Asp Phe Glu Val Thr 205 acg gcg ttt cga gcg cta cgt gac ttc ttt gag gat ccg gaa gaa att 787 Thr Ala Phe Arg Ala Leu Arg Asp Phe Phe Glu Asp Pro Glu Glu Ile 220

gct gag tac atg atg gac gtc atg atg gac aac aag ggg gag tcc

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832

235 240

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855

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Lys Arg Met Leu Asp Phe Arg Ala Pro Ile Thr Val Ile Thr Gly Glu 35 40 45

Asn Gly Val Gly Lys Ser Thr Leu Leu Glu Ala Ile Ala Ile Asn Ala 50 55 60

Gly Phe Asp Thr Ala Gly Gly Glu His Thr Gly Lys Phe Lys Pro Ser 65 70 75 80

Asp Asn Pro Leu Gln Thr Val Ala Lys Ala His Lys Gly Lys Glu Pro
85 90 95

Gly Tyr Arg Asp Glu Ala Pro Gly Trp Val Asn Leu His His Met Ser 115 120 125

His Gly Glu Ser Val Met His Ile Val Gln Asn Ala Phe Val Gly Lys

Gly Leu Tyr Leu Met Asp Glu Pro Glu Ala Gly Leu Ser Phe Ile Arg 145 150 155 160

Gln Met Ala Ile Leu Ala Glu Leu Asn Phe Leu Ala Glu Ser Gly Ala 165 170 175

Gln Ile Ile Val Thr His Ser Pro Val Leu Met Ala Ile Pro Gly
180 185 190

Ala Glu Ile Trp Glu Phe Ser Ala Ser Gly Glu Leu His Arg Gly Phe 195 200 205

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Lys Gly Glu Ser

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					caa Gln											739
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					cca Pro											931
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					cgt Arg											1027
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tcg Ser	ggc Gly	att Ile	gag Glu	aac Asn 330	tat Tyr	tct Ser	cgc Arg	cac His	att Ile 335	gat Asp	gga Gly	cgt Arg	GJA āāā	gag Glu 340	gga Gly	1123
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					cac His											1219
					cgt Arg											1267
					gat Asp 395											1315
					acg Thr											1363
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2220

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565 570 575

Asp Lys Ile Thr Asp Ser Met Gln Tyr Ala Ile Glu Glu Thr Asp Arg 580 585 590

Arg Arg Glu Lys Gln Val Ala Tyr Asn Lys Glu His Gly Ile Asp Pro 595 600 605

Gln Pro Leu Arg Lys Lys Ile Ala Asp Ile Leu Asp Gln Val Tyr Asp 610 620

Asn Ser Ala Asp Gly Ala Gly Pro Ser Ala Ser Gly Asp Ala Ala Val 625 635 640

Val Ala Lys Pro Asp Val Ser Ser Met Pro Ala Lys Glu Val Gln Lys 645 650 655

Leu Ile Asp Asp Leu Ser Ala Gln Met Ala Ala Ala Ala Arg Glu Leu 660 665 670

Lys Phe Glu Leu Ala Gly Arg Leu Arg Asp Glu Ile Phe Glu Leu Lys 675 680 685

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Met Thr Ser Arg Asp

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gct tta acc aca gac gaa ctt gaa gca ctc aac aac gcc aat tat ggc 211
Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn Asn Ala Asn Tyr Gly
25 30 35

ctc gac cgc aat ctg ggg ctg cgc tac acc acc atc gag ccc ggc cgg Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr Ile Glu Pro Gly Arg 40 45 50

gtg gtc agc gaa ctt cac gtg gca tcc aag cac ctg caa gtg gtg ggc 307 Val Val Ser Glu Leu His Val Ala Ser Lys His Leu Gln Val Val Gly 55 60 65

ttg gtc aac ggt ggt gtc tac gcc gcc atc gcc gaa tcc act gga tca 355

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Met 1 Leu Asn Ile Leu 65 Glu Val Gly	Thr Ala Ala Glu 50 Gln Ser Val	Ala Asn 35 Pro Val Thr Gly Ile 115	Thr 20 Tyr Gly Val Gly Ile 100 Val	5 Arg Gly Arg Gly Ser 85 Asn	Ala Leu Val Leu 70 Val Asn	Leu Asp Val 55 Val Ala Asn	Thr Arg 40 Ser Asn Ser Thr	Thr 25 Asn Glu Gly Met Asp 105 Pro	10 Asp Leu Leu Gly Ile 90 Phe	Glu Gly His Val 75 Ser Ile	Leu  Val 60 Tyr Ala Ser	Glu Arg 45 Ala Ala Pro Ala Gly 125	Ala 30 Tyr Ser Ala Gly Val 110 Gly	15 Leu Thr Lys Ile Lys 95 Ser Arg	Asn Thr His Ala 80 Met Ser

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GIC	i ASI.	ıtyr	GIN	10	Pro	Ala	Pro	Ser	Ser 15	Gln	Val	Val	Val	Ser 20		163
val	GIY	HIS	25	Ala	Lys	Pro	Gly	Leu 30	Val	Thr	Leu	Ala	Glu 35	Gly		211
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Leu Pro Asp Ala Asp Leu Thr Ala Leu Asn Leu Ala Gln Leu Leu Val 50 55 60

Asp Gly Thr Gln Ile His Val Leu Ala Ile Gly Glu Val Gln Pro Ile 65 70 75 80

Ser Val Asp Ala Ala Thr Ser Ala Ser Gly Leu Ile Ser Leu Asn 85 90 95

Thr Ala Thr Val Ala Asp Leu Val Thr Leu Pro Gly Val Gly Glu Lys
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gcg ctc aac ttg gcg caa ttg ctt gtc gac ggc acc cag atc cat gtt  $\,$  259 Ala Leu Asn Leu Ala Gln Leu Leu Val Asp Gly Thr Gln Ile His Val

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135

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105 110

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Ile Lys Pro Asp Ser Phe Pro Gly Val Gly Asp Leu Thr Ile Ser Thr 135

Glu Asp Ile Asp Gln Leu Glu Pro Thr Thr Gly Tyr Ser Ala Trp Val

Asn Gln Val Arg Asp Gly Phe Ser Gln Ala Val Glu Glu Thr Val Gly 170

Glu Ser Ser Arg Gly Leu Ile Pro Gly Met Val Leu Gly Asp Thr Arg 185

Leu Gln Gly Ser Ile Glu Ala Gln Thr Tyr Ile Asp Thr Gly Leu Ser 200

His Leu Ser Ala Val Ser Gly Ser Asn Val Ala Ile Val Val Ser Ser 215

Val Val Val Leu Ser Tyr Phe Leu Thr Ala Gly Pro Arg Ile Arg Val

Val Ala Ser Leu Leu Ser Leu Val Ile Phe Val Ser Leu Val Gly Phe 250

Glu Pro Ser Val Leu Arg Ala Ser Val Thr Gly Ile Val Gly Leu Leu 265

Ala Ile Ile Asn Ser Ser Arg Met Glu Pro Met His Gly Leu Ser Leu 280

Ser Val Ile Cys Leu Leu Phe Tyr Asp Ser Asn Leu Ala Val His Tyr

Gly Phe Leu Leu Ser Cys Ala Ala Thr Ala Gly Ile Val Met Leu Gln 315

Pro Leu Leu Tyr Arg Ala Ile Gly Pro Pro Leu Ala Val Trp Lys Val

Pro Asp Ile Val Val Arg Ala Phe Ala Val Ser Ile Ala Ala Asp Leu 345

Val Thr Ile Pro Ile Ile Ala Leu Met Ala Arg Gln Ile Ser Leu Val

Ala Val Leu Ala Asn Val Leu Val Glu Leu Ala Val Pro Pro Ile Thr 380

Leu Leu Gly Leu Ile Ala Val Leu Ala Ser Leu Leu Pro Trp Pro Val

Glu Tyr Pro Leu Leu Lys Ile Ile Glu Pro Phe Thr Trp Trp Ile His 410

His Val Ala Lys Trp Cys Gln Gln Leu Pro Asn Ser Thr Leu Glu Ile

Ser Ala Gly Trp Ala Gly Ile Ala Trp Ala Cys Met Ala Ala Val Trp

440 Val Val Val Ile Ile Tyr Lys Gly Tyr Val Arg Thr Leu Ala Val Cys Cys Val Cys Phe Phe Leu Phe Gly Ala Trp Asn Asn Arg Leu Pro Ala Gln Ile Asp Pro Thr Glu Leu Arg Phe Val Ile Ile Ala Asp Asp Ser 490 Glu Leu Thr Asp Val Pro Glu His Ala Glu Leu Ile Ile Val Glu Asp 505 Pro His Gly Ser Met Ser Asp Arg Pro Ile Val Thr Arg Glu Gly Ile 520 Pro Val Leu Tyr Pro Tyr Arg Asp Gly Glu Val Ser Leu His Ile Asp 535 Gly Thr Gln His Ala Ala Asp Gly Arg Phe 550 <210> 113 <211> 871 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(871) <223> FRXA02385 <400> 113 ttcgggagag caacggtggg tttagcaccg tggaggattt actgcaggtc aaggggattg 60 ggccctcaaa gtttgagcag atctctggat tggtgtcccc atg att gag gtg cgt 115 Met Ile Glu Val Arg ttg gtt ccc gtg gcg gct gtg atg tgg atg gct gtc gct gcg ttg att 163 Leu Val Pro Val Ala Ala Val Met Trp Met Ala Val Ala Ala Leu Ile 1.0 atc aat ggt tcg tgg gtg ttg tcg gtg ggg att gtt ggc atc gcg atc 211 Ile Asn Gly Ser Trp Val Leu Ser Val Gly Ile Val Gly Ile Ala Ile att gct gct tgt gtg ttt aaa cac tgg ggt caa gct gtg gtg ata gct 259 Ile Ala Ala Cys Val Phe Lys His Trp Gly Gln Ala Val Val Ile Ala gca ctg ggc gtt ggt gcc gta gtg atg gct gcg ttg aga atc agc agc 307 Ala Leu Gly Val Gly Ala Val Val Met Ala Ala Leu Arg Ile Ser Ser gcg aag gca ttt gaa gca ccg caa acc tgg gtg ggt acc gca gaa acc 355 Ala Lys Ala Phe Glu Ala Pro Gln Thr Trp Val Gly Thr Ala Glu Thr

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Ser Val Ile Cys Leu Leu Phe Tyr Asp Ser Asn Leu Ála Val His Tyr

96

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869

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caa	agc	aat	aaa	acc	t c =	020	¬+~	~+ ~								
C 1	~ 5 -	220		acc	LCa	Cac	alg	crg	gga	att	atc	gca	gat	tgc	ctc	307
GIN	Ser	GLy	Lys	Thr	Ser	His	Met	Len	G1v	Tla	Tla	ת ו ת	7 00	Cira	Leu	
	5.5		-						O L y	116	TIG	Ата	ASP	Cys	ьeu	
	55					60					65					

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<213> Corynebacterium glutamicum

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His Thr Val Met Asp Asp Phe Asp Tyr Ile Ser Asp Gln Gln Val Leu 35 40 45

Leu Tyr Gly Asp Val Gln Ser Gly Lys Thr Ser His Met Leu Gly Ile 50 60

Ile Ala Asp Cys Leu Asp Ser Thr Phe His Thr Ile Val Ile Leu Thr 65 70 75 80

Ser Pro Asn Thr Arg Leu Val Gln Gln Thr Tyr Asp Arg Val Ala Gln  $85 \\ 90 \\ 95$ 

Ala Phe Pro Asp Thr Leu Val Cys Asp Arg Asp Gly Tyr Asn Asp Phe 100 105 110

Arg Ala Asn Gln Lys Ser Leu Thr Pro Arg Lys Ser Ile Val Val Val 115

Gly Lys Ile Pro Ala Val Leu Gly Asn Trp Leu Arg Val Phe Asn Asp 130 135 140

Ser Gly Ala Leu Ser Gly His Pro Val Leu Ile Ile Asp Asp Glu Ala 145 150 155 160

Asp Ala Thr Ser Leu Asn Thr Lys Val Asn Gln Ser Asp Val Ser Thr 165 170 175

Ile Asn His Gln Leu Thr Ser Ile Arg Asp Leu Ala Thr Gly Cys Ile 180 185 190

Tyr Leu Gln Val Thr Gly Thr Pro Gln Ala Val Leu Leu Gln Ser Asp 195 200 205

Asp Ser Asn Trp Ala Ala Glu His Val Leu His Phe Ala Pro Gly Glu 210 215 220

Ser Tyr Ile Gly Gly Gln Leu Phe Phe Ser Glu Leu Asn Asn Pro Tyr 230 235 240

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Gly Glu Ser Leu Cys Thr Met Leu Ile His Pro Ser His Thr Ala Ser

275 280 285 Ser His Arg Asp Phe Ala Gln Glu Ala Arg Leu Gln Leu Thr Phe Ala 295 300 Phe Glu Arg Phe Tyr Glu Pro Met Ile Gln His Asn Phe Gln Arg Ala 315 Tyr Glu Gln Leu Ala Gln Thr Asp Ser Asn Leu Pro Pro Leu Arg Lys 330 Ile Leu Asn Ile Leu Gly Gly Met Glu Asp Asp Phe Ser Ile His Ile 345 Val Asn Ser Asp Asn Pro Thr Val Glu Glu Asp Trp Ala Asp Gly Tyr 360 Asn Ile Ile Val Gly Gly Asn Ser Leu Gly Arg Gly Leu Thr Phe Asn 375 Asn Leu Gln Thr Val Phe Tyr Val Arg Glu Ser Lys Arg Pro Gln Ala 390 Asp Thr Leu Trp Gln His Ala Arg Met Phe Gly Tyr Lys Arg His Lys 405 Asp Thr Met Arg Val Phe Met Pro Ala Thr Ile Ala Gln Thr Phe Gln 425 Glu Val Tyr Leu Gly Asn Glu Ala Ile Lys Asn Gln Leu Asp His Gly Thr His Ile Asn Asp Ile Arg Val Ile Leu Gly Asp Gly Val Ala Pro 455 Thr Arg Ala Asn Val Leu Asp Lys Arg Lys Val Gly Asn Leu Ser Gly Gly Val Asn Tyr Phe Ala Ala Asp Pro Arg Ile Lys Asn Val Glu Ala 490 Leu Asp Lys Lys Leu Leu Ala Tyr Leu Asp Lys His Gly Glu Asp Ser 505 Thr Ile Gly Met Arg Ala Ile Ile Thr Ile Leu Asn Ala Phe Thr Val 520 Asp Pro Asn Asp Leu Asp Leu Ala Thr Phe Lys Ala Ala Leu Leu Asp 535 Phe Glu Arg Asn Gln Pro His Leu Thr Ala Arg Met Val Leu Arg Thr 550 Asn Arg Lys Val Asn Gln Gly Thr Gly Ala Leu Leu Ser Pro Thr Asp 565 Gln Ala Leu Ser Arg Ala Glu Val Ala His Pro Leu Leu Ile Leu Tyr Arg Ile Glu Gly Val Asn Asp Ala Ala Ala Gln Arg Gly Glu Pro Thr 600

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gcg ag Ala Ar 70															355
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tgt cg Cys Ar			_	_	_	_	_				-			-	451
gag ca Glu Hi	_	Val		-	_			_		_	_			-	499
gaa to Glu Se 13	r Thr														547

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cg Ar	a ga g As	c at p Me	g gc t Al 18	a AS	t gc p Al	t ga a Gl	a ggg	g gaa 7 Glu 190	ı Lev	g caq ı Glr	g agg n Arg	g cct g Pro	cga Arg	g Trp	aag Lys	691
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ato Me	g tto E Pho 21!	- <u>- y</u>	t cc r Pr	g gt o Va	g tg l Tr	g tto Phe 220	e Asp	gag Glu	tcg Ser	act Thr	ggg Gly 225	cga Arg	ctc	agc Ser	cac His	787
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Pro	Phe	His 35	Thr	Val	Val	Asn	Ala 40	Glu	Asn	Tyr	His	Ala 45	Leu	Glu	Met	
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Pro 65	Tyr	Asn	Thr	Gly	Ala 70	Arg	Asp	Trp	Lys	Tyr 75	Asp .	Asn <i>i</i>	Asp	Tyr '	Val 80	
Ala	Ser	Asp	Asp	Asp 85	Tyr	Arg	His	Ser	Lys ' 90	Trp	Leu <i>i</i>	Ala 1	Phe	Met (	Glu	

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					•											
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Asp Glu Ile Ile Gly Lys Thr Lys Val Ser Ala Leu Leu Glu Ala Leu

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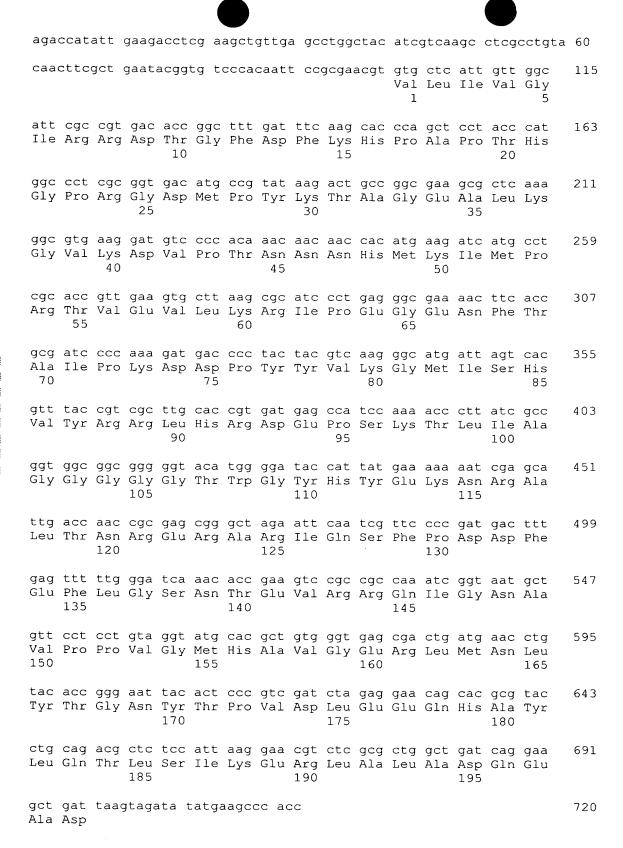
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Gly Met Ile Ser His Val Tyr Arg Arg Leu His Arg Asp Glu Pro Ser 85 90 95

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Glu Lys Asn Arg Ala Leu Thr Asn Arg Glu Arg Ala Arg Ile Gln Ser 115 120 125

Phe Pro Asp Asp Phe Glu Phe Leu Gly Ser Asn Thr Glu Val Arg Arg 130 135 140

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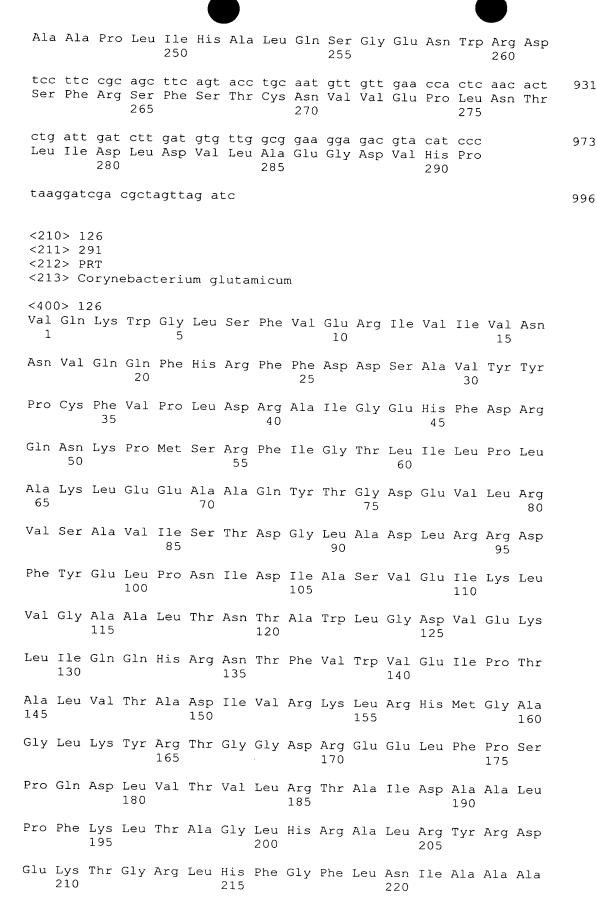
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gct Ala 230	gga Gly	aaa Lys	ggc Gly	Glu	gca Ala 235	gag Glu .	gca Ala	ctg Leu	Lys	atc Ile 240	ctt Leu	gaa Glu	ggc Gly	gat Asp	gat Asp 245	835
gcc	gct	ccg	ctt	att	cac	gca (	cta	caa	agc	ggc	gaa	aac	tgg	cgg	gat	883



Val Ala Thr Leu Arg Ala Gly Lys Gly Glu Ala Glu Ala Leu Lys Ile 235 Leu Glu Gly Asp Asp Ala Ala Pro Leu Ile His Ala Leu Gln Ser Gly 245 250 Glu Asn Trp Arg Asp Ser Phe Arg Ser Phe Ser Thr Cys Asn Val Val 265 Glu Pro Leu Asn Thr Leu Ile Asp Leu Asp Val Leu Ala Glu Gly Asp 280 Val His Pro 290 <210> 127 <211> 729 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(706) <223> RXN02988 <400> 127 agcggcaaat atgtgcggct tggcataaac tgtgtccatc ggtacctgtg taatagacac 60 acggtaaaca cgcacaagat aaaacattgc gagatttttc atg agt aca aaa ccc Met Ser Thr Lys Pro 1 act att gtg tcc aca ttt tct ggt tgc ggt ggc ctc gat ctt ggc ctc 163 Thr Ile Val Ser Thr Phe Ser Gly Cys Gly Gly Leu Asp Leu Gly Leu 10 caa gag gtc gga ttc gac ccc att tgg gcc aac gac ttc tca gaa gaa 211 Gln Glu Val Gly Phe Asp Pro Ile Trp Ala Asn Asp Phe Ser Glu Glu 30 gca gtc caa acc tat aag cac aac atc ggt gac cac att gtt cac ggc 259 Ala Val Gln Thr Tyr Lys His Asn Ile Gly Asp His Ile Val His Gly 40 45 gac atc act gaa att gat ccg ttt act gat gac acc atc cct gac ggc 307 Asp Ile Thr Glu Ile Asp Pro Phe Thr Asp Asp Thr Ile Pro Asp Gly 55 60 gat etc gtc acc ggc ggc ttc ecg tgc eag gac ttc tec atg atc tgg Asp Leu Val Thr Gly Gly Phe Pro Cys Gln Asp Phe Ser Met Ile Trp 70 75 80 aag cgt cct gga ctc gac ggc aag cgt ggc acc ctg tac caa aac ttc Lys Arg Pro Gly Leu Asp Gly Lys Arg Gly Thr Leu Tyr Gln Asn Phe 90 cgt gac ttt gtt gca gca aag aag cct aaa gcc ttt atc gca gaa aac 451 Arg Asp Phe Val Ala Ala Lys Lys Pro Lys Ala Phe Ile Ala Glu Asn 105

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	aag Lys 135															547
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Leu Asp His Thr 65	Asp Phe Ile 50	Thr Leu Ser 35 Val Pro	Gly 20 Glu His	5 Leu Glu Gly	Gln Ala Asp Asp	Glu Val Ile 55 Leu	Val Gln 40 Thr	Gly 25 Thr Glu Thr	10 Phe Tyr Ile Gly	Asp  Asp  Gly 75	Pro His Pro 60 Phe	Ile Asn 45 Phe	Trp 30 Ile Thr	15 Ala Gly Asp	Asn Asp Asp Asp	
Leu Asp His Thr 65	Asp Phe Ile 50	Thr Leu Ser 35 Val Pro	Gly 20 Glu His Asp	5 Leu Glu Gly Gly	Gln Ala Asp Asp 70 Lys	Glu Val Ile 55 Leu Arg	Val Gln 40 Thr Val	Gly 25 Thr Glu Thr	10 Phe Tyr Ile Gly Leu 90	Asp  Asp  Gly 75  Asp	Pro His Pro 60 Phe	Ile Asn 45 Phe Pro	Trp 30 Ile Thr Cys	Ala Gly Asp Gln Gly 95	Asn Asp Asp Arp Asp Thr	
Leu Asp His Thr 65 Phe Leu	Asp Phe Ile 50 Ile Ser	Thr Leu Ser 35 Val Pro Met	Gly 20 Glu His Asp Ile Asn 100	5 Leu Glu Gly Trp 85 Phe	Gln Ala Asp 70 Lys Arg	Glu Val Ile 55 Leu Arg	Val Gln 40 Thr Val Pro	Gly 25 Thr Glu Thr Gly Val 105	10 Phe Tyr Ile Gly Leu 90 Ala	Asp Lys Asp Gly 75 Asp	Pro His Pro 60 Phe Gly Lys	Ile Asn 45 Phe Pro Lys	Trp 30 Ile Thr Cys Arg Pro 110	Ala Gly Asp Gln Gly 95 Lys	Asn Asp Asp Asp Thr	
Leu Asp His Thr 65 Phe Leu Phe	Asp Phe Ile 50 Ile Ser Tyr	Thr Leu Ser 35 Val Pro Met Gln Ala 115	Gly 20 Glu His Asp Ile Asn 100 Glu	5 Leu Glu Gly Gly Trp 85 Phe Asn	Gln Ala Asp 70 Lys Arg Val	Glu Val Ile 55 Leu Arg Asp	Val Gln 40 Thr Val Pro Phe Gly 120	Gly 25 Thr Glu Thr Gly Val 105 Leu	10 Phe Tyr Ile Gly Leu 90 Ala Leu	Asp Lys Asp Gly 75 Asp Ala	Pro His Pro 60 Phe Gly Lys Ala	Ile Asn 45 Phe Pro Lys Lys Asn 125	Trp 30 Ile Thr Cys Arg Pro 110 Gln	Ala Gly Asp Gln Gly 95 Lys	Asn Asp Asp 80 Thr Ala	

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Pro	Val	Glu	Arg	Val	Cys	Asn	Ala	Ser	Arq	Leu	Ser	Thr	Phe	Pro	Cvs	
70					7.5				_	80					0.5	

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ctt ( Leu ( 150	3 <b>.</b> Y	пт2	itb	HIS	155	Pro	Ser	Pro	Val	Ala 160	Val	Ala	Ser	Pro	His 165	595
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Leu Gly Asp Thr Asp Ser Glu Lys Arg Ala Ala Val Leu Met Leu Phe 50 60

Ser Gly Ser Glu Thr Ser Phe Asp Leu Pro Asn Asp Ala Ser Val Leu 65 70 75 80

Leu Thr His Arg Thr Pro Thr Met Arg Ser His Ala Gly Gln Ile Ala 85 90 95

Phe Pro Gly Gly Arg Ile Asp Pro Thr Asp Thr Asn Ala Val Asp Cys
100 105 110

Ala Phe Arg Glu Ala Trp Glu Glu Thr Gly Leu Asp Arg Arg Thr Ala 115 120 125

Thr Pro Leu Ala Gln Leu Asn Glu Val His Ile Arg Ala Thr Gly Tyr 130 140

Pro Val Tyr Pro Ile Leu Gly His Trp His Thr Pro Ser Pro Val Ala 145 150 155 160

Val Ala Ser Pro His Glu Thr Asp Glu Val Leu Asp Ala Pro Leu Tyr 165 170 175

Asp Leu Ile Asp Pro Lys Asn Arg Leu Met Val Gly Trp Arg Glu Trp 180 185 190

His Gly Pro Ala Phe Arg Ile Asn Asp Tyr Ile Ile Trp Gly Phe Thr 195 200 205

Gly Gly Leu Leu Ser Ala Ile Leu Asp Thr Ala Gly Trp Ala Thr Glu 210 215 220

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	- 100	4 11IC	r riie	15	)	ser	. ren	Thr	. Ala 20	Gly	' Leu	Ala	Ser	Ala 25		160
		. 010	30	i FIC	, GIA	Ala	ser	35	Val	Leu	Lys	Gly	Gly 40	Leu		208
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Lys Val Ala Leu Ala Gly Val Pro Gln Glu Leu Ile Asp Ala His Gly

Val Val Ser Pro Gln Cys Ala Arg Ala Met Ala Thr Gly Ala Ala His

Arg Cys Gln Ala Asp Trp Ala Val Ser Leu Thr Gly Val Ala Gly Pro

Ser Lys Gln Asp Gly His Pro Val Gly Glu Val Trp Ile Gly Val Ala 105

Gly Pro Ala His Phe Gly Ala Ser Gly Thr Ile Asp Ala Tyr Arg Ala 120

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aat gtt gtg ttc aat gcg cat cac ccc aaa gat acg cag ccg ttg gat 163 Asn Val Val Phe Asn Ala His His Pro Lys Asp Thr Gln Pro Leu Asp 15

aag ttc ttc gat aaa gaa ctt aaa gac aca cat cat ctc gat ata acg Lys Phe Phe Asp Lys Glu Leu Lys Asp Thr His His Leu Asp Ile Thr

25 30 35 gtg ggt tat atc agt gag aaa tca cta caa tat ttg ctt ctt att gca 259 Val Gly Tyr Ile Ser Glu Lys Ser Leu Gln Tyr Leu Leu Ile Ala ggc act tac ccc gac ctc acc att aca ctt acc tgt gga atg cac gct 307 Gly Thr Tyr Pro Asp Leu Thr Ile Thr Leu Thr Cys Gly Met His Ala cgt gaa ggc atg act gct gcc caa ctg cat cat gcg cga gtg ctc cat 355 Arg Glu Gly Met Thr Ala Ala Gln Leu His His Ala Arg Val Leu His gac tac tta agc gac cat gat cga ggc ggg gtg ttc gtt att ccc cga 403 Asp Tyr Leu Ser Asp His Asp Arg Gly Gly Val Phe Val Ile Pro Arg 95 ttg cgt tat cac ggg aaa atc tat ctt ttc cac aag aac cag cac aca 451 Leu Arg Tyr His Gly Lys Ile Tyr Leu Phe His Lys Asn Gln His Thr 105 110 gat cct att gct tat atc ggt agc gct aac ctc tca gcc atc gtt cct 499 Asp Pro Ile Ala Tyr Ile Gly Ser Ala Asn Leu Ser Ala Ile Val Pro 120 125 130 ggg tac acc tet aca tte gag eee gge gte ate tta gae eee gea eet 547 Gly Tyr Thr Ser Thr Phe Glu Pro Gly Val Ile Leu Asp Pro Ala Pro 135 gaa gat ctc gtg ctt cat ctc aac cgt gat gtc gta ccc cta tgt gtc 595 Glu Asp Leu Val Leu His Leu Asn Arg Asp Val Val Pro Leu Cys Val 150 155 ccc att gac acc gcg cat gtc ccc atc att aaa gat caa gaa tcc ccg 643 Pro Ile Asp Thr Ala His Val Pro Ile Ile Lys Asp Gln Glu Ser Pro 170 atg aag cac gtc gct gaa gca aca gct gtg tcc acc tct gat gtt gtt 691 Met Lys His Val Ala Glu Ala Thr Ala Val Ser Thr Ser Asp Val Val 185 190 gee ate atg tee age eea ttt act tat agt ttt gae ett aaa ete aaa 739 Ala Ile Met Ser Ser Pro Phe Thr Tyr Ser Phe Asp Leu Lys Leu Lys 200 gcc act gcc agc agc aac ctc aat gct cat aac tca ggc ggt ggc gcg 787 Ala Thr Ala Ser Ser Asn Leu Asn Ala His Asn Ser Gly Gly Ala 215 cgc aaa cag aaa aac ggt agc ttc ctt gca cgc aat tgg tat gag ggc 835 Arg Lys Gln Lys Asn Gly Ser Phe Leu Ala Arg Asn Trp Tyr Glu Gly 230 235 gaa atc att gtc ggt gtc gag aca aca aga ctc cca ggt tac cca caa Glu Ile Ile Val Gly Val Glu Thr Thr Arg Leu Pro Gly Tyr Pro Gln 250 aac aaa tcc gaa ttc act gcg ggt cac tgatgacggc tggtcatttg 930 Asn Lys Ser Glu Phe Thr Ala Gly His 265

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Cys Gly Met His Ala Arg Glu Gly Met Thr Ala Ala Gln Leu His His

Ala Arg Val Leu His Asp Tyr Leu Ser Asp His Asp Arg Gly Gly Val

Phe Val Ile Pro Arg Leu Arg Tyr His Gly Lys Ile Tyr Leu Phe His

Lys Asn Gln His Thr Asp Pro Ile Ala Tyr Ile Gly Ser Ala Asn Leu

Ser Ala Ile Val Pro Gly Tyr Thr Ser Thr Phe Glu Pro Gly Val Ile 135

Leu Asp Pro Ala Pro Glu Asp Leu Val Leu His Leu Asn Arg Asp Val 155

Val Pro Leu Cys Val Pro Ile Asp Thr Ala His Val Pro Ile Ile Lys

Asp Gln Glu Ser Pro Met Lys His Val Ala Glu Ala Thr Ala Val Ser 185

Thr Ser Asp Val Val Ala Ile Met Ser Ser Pro Phe Thr Tyr Ser Phe 200

Asp Leu Lys Leu Lys Ala Thr Ala Ser Ser Asn Leu Asn Ala His Asn 210 215

Ser Gly Gly Gly Ala Arg Lys Gln Lys Asn Gly Ser Phe Leu Ala Arg 230

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cgt c Arg L 310	tt o eu <i>F</i>	gcg . Ala '	act Thr	var i	cca Pro 2 315	gca d Ala H	cca ( Pro (	gag Glu	cct Pro	gcg Ala 320	atc Ile	att Ile	cgg Arg	gtt Val	cgc Arg 325	1075
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Met Gly Val Ala Phe Gly Ile Thr Ala Leu Gly Ala Ser Gly Leu Thr 180 185 190

Lys Asn Leu Leu Asp Phe Val Gly Leu Gly Glu Ile Pro Gly Ile Ser 195 200 205

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Val Val Lys Gln Val Gly Ser Leu Leu Ala Ser Asn Ala Leu Ser Asn 260 265 270

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Leu Leu Thr Arg Gln Gln Val Asp Ala Ile Ile Arg Ser Ala Glu 85 90 95

Gly Ala His Arg Arg Leu Leu Lys Asp Gly Arg Gly Ala Arg Thr Val  $100 \\ 105 \\ 110$ 

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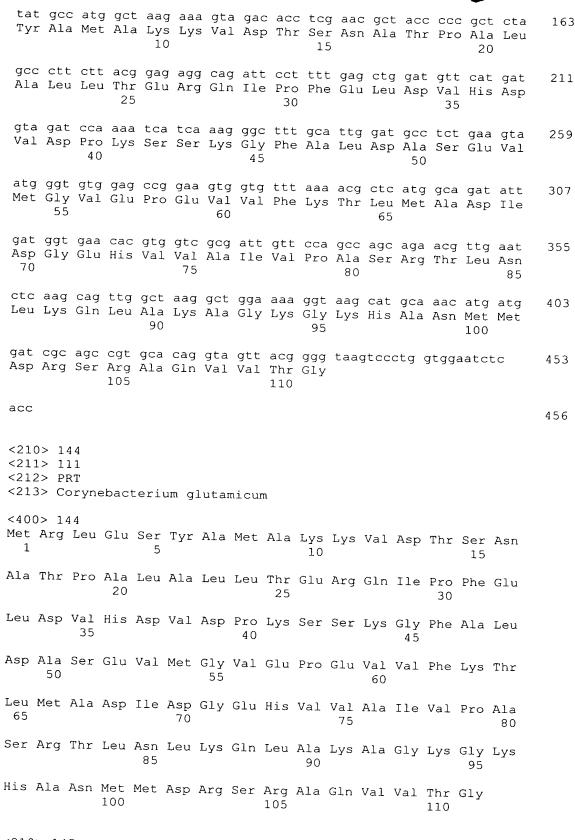
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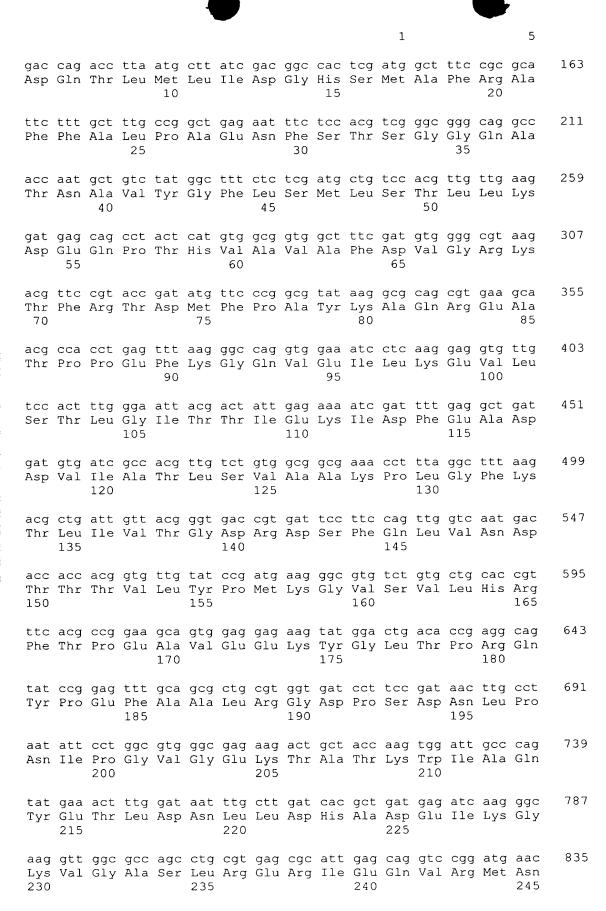
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 Ser Ala Ile Leu Gln Glu Arg Ile Tyr Val Ser Ala Gly Arg Arg Gly
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 Trp Ser Leu Ile Ile Ala Pro Asp Asp Val Leu Leu Ala Thr Asp Gly
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Ala Gly Arg Arg Gly Trp Ser Leu Ile Ile Ala Pro Asp Asp Val Leu
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	gtg Val 295	_	_	_			-	-				_				1027
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gta /al	cag Gln	cgc Arg 760	tac Tyr	ctc Leu	cgg Arg	gag Glu	atc Ile 765	gtg Val	gag Glu	gag Glu	gct Ala	cga Arg 770	aaa Lys	gct Ala	ggc Gly	2419
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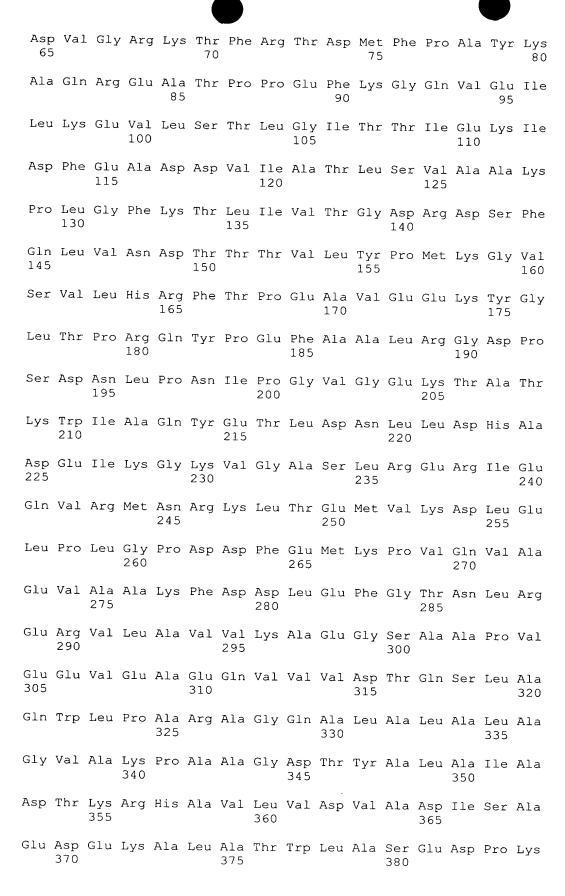
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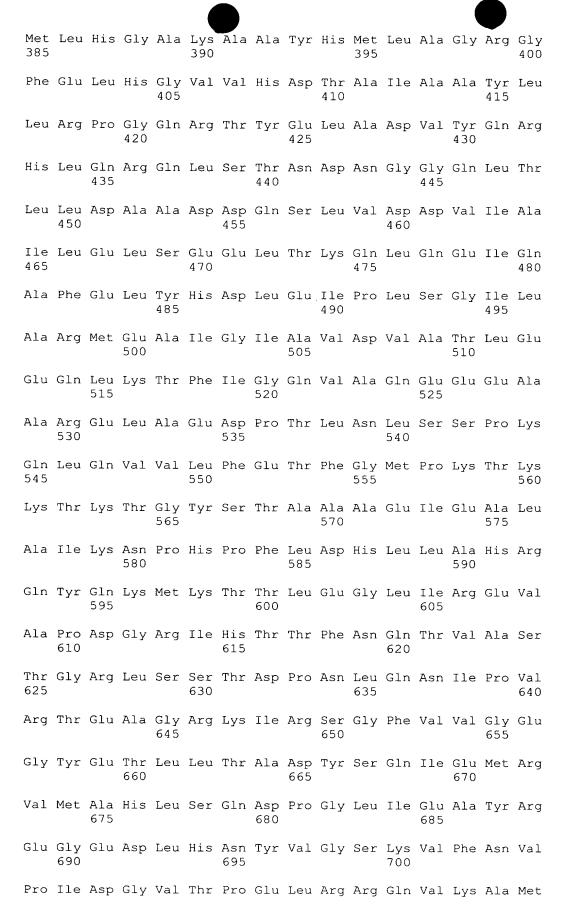
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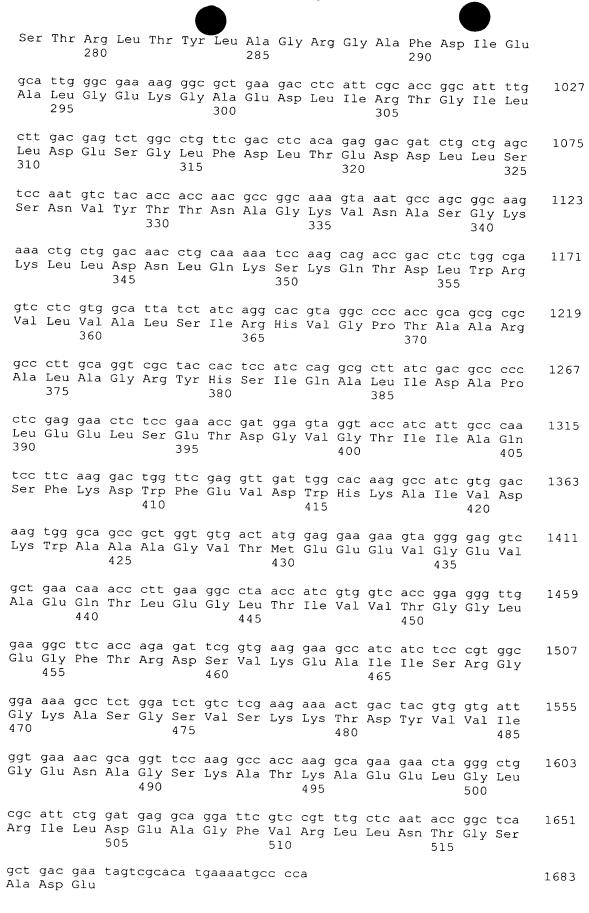
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BGI-127CP - 205 -



705 710 715 720 Ser Tyr Gly Leu Val Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln 730 Leu Ser Ile Pro Ala Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe Glu Arg Phe Gly Gly Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu 760 Ala Arg Lys Ala Gly Tyr Thr Glu Thr Leu Phe Gly Arg Arg Tyr 775 Leu Pro Glu Leu Thr Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu Arg Ala Ala Leu Asn Ala Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Val Ala Met Ile Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val 825 Lys Ser Arg Val Leu Leu Gln Val His Asp Glu Leu Val Val Glu Val 840 Ala Ala Gly Glu Leu Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met 855 Asp Asn Ala Ile Lys Leu Ser Val Pro Leu Glu Val Ser Ala Gly Asp 870 875 Gly Val Asn Trp Asp Ala Ala Ala His 885 <210> 149 <211> 1683 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1660) <223> RXS00212 <400> 149 ttagagcgtg ccgctactcg tggtgatggt cgcgtgggcg aggacatcac ggccaatgct 60 egegtgateg aagatateee geaceagett cagggeactg atg aat ate etg tge 115 Met Asn Ile Leu Cys ctg ctg tgc tgg aaa ttc gcg gtg agg tgt tca tca ctg tgg agg att Leu Leu Cys Trp Lys Phe Ala Val Arg Cys Ser Ser Leu Trp Arg Ile 163 tee cag gag gte aac geg cag ege att get gat gge gge aag eeg ttt Ser Gln Glu Val Asn Ala Gln Arg Ile Ala Asp Gly Gly Lys Pro Phe 211 25 30 35

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520

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<212> PRT

<213> Corynebacterium glutamicum

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Gly Gly Lys Pro Phe Ala Asn Pro Arg Asn Ala Ala Gly Ser Leu 35 40 45

Arg Gln Lys Asn Ile Glu Asp Val Lys Lys Arg Arg Leu Arg Met Ile 50 55 60

Ser His Gly Ile Gly Phe Thr Glu Gly Phe Ser Pro Ala Ser Gln His 65 70 75 80

Asp Ala Tyr Leu Ala Leu Ala Ala Trp Gly Leu Pro Thr Ser Pro Tyr 85 90 95

Thr Glu Ala Val Thr Asp Pro Glu Asp Val Val Lys Lys Val Ser Tyr
100 105 110

Trp Ala Asp His Arg His Asp Ala Leu His Glu Met Asp Gly Leu Val 115 120 125

Ile Lys Val Asp Asp Ile Ala Ser Gln Arg Ala Leu Gly Ser Thr Ser 130 135 140

Arg Ala Pro Arg Trp Ala Ile Ala Tyr Lys Tyr Pro Pro Glu Glu Val 145 150 155 160

Thr Thr Lys Leu Leu Asp Ile Gln Val Gly Val Gly Arg Thr Gly Arg 165 170 175

Val Thr Pro Phe Ala Val Met Glu Pro Val Leu Val Ala Gly Ser Thr 180 185 190

Val Ser Met Ala Thr Leu His Asn Gln Ser Glu Val Lys Arg Lys Gly
195 200 205

Val Leu Ile Gly Asp Thr Val Val Ile Arg Lys Ala Gly Glu Val Ile 210 215 220

Pro Glu Val Leu Gly Pro Val Val Glu Leu Arg Asp Gly Thr Glu Arg 225 230 235 240

Glu Tyr Ile Phe Pro Thr Leu Cys Pro Glu Cys Gly Thr Arg Leu Ala 245 250 250

Pro Ala Lys Ala Asp Asp Val Asp Trp Arg Cys Pro Asn Met Gln Ser 260 265 270

Cys Pro Gly Gln Leu Ser Thr Arg Leu Thr Tyr Leu Ala Gly Arg Gly

275 280 285

Ala Phe Asp Ile Glu Ala Leu Gly Glu Lys Gly Ala Glu Asp Leu Ile 290 295 300

Arg Thr Gly Ile Leu Leu Asp Glu Ser Gly Leu Phe Asp Leu Thr Glu 305 310 315

Asp Asp Leu Leu Ser Ser Asn Val Tyr Thr Thr Asn Ala Gly Lys Val 325 330 335

Asn Ala Ser Gly Lys Lys Leu Leu Asp Asn Leu Gln Lys Ser Lys Gln 340 345 350

Thr Asp Leu Trp Arg Val Leu Val Ala Leu Ser Ile Arg His Val Gly 355 360 365

Pro Thr Ala Ala Arg Ala Leu Ala Gly Arg Tyr His Ser Ile Gln Ala 370 380

Leu Ile Asp Ala Pro Leu Glu Glu Leu Ser Glu Thr Asp Gly Val Gly 385 390 395 400

Lys Ala Ile Val Asp Lys Trp Ala Ala Ala Gly Val Thr Met Glu Glu 420 425 430

Glu Val Gly Glu Val Ala Glu Gln Thr Leu Glu Gly Leu Thr Ile Val 435 440 445

Val Thr Gly Gly Leu Glu Gly Phe Thr Arg Asp Ser Val Lys Glu Ala 450 455 460

Ile Ile Ser Arg Gly Gly Lys Ala Ser Gly Ser Val Ser Lys Lys Thr 465 470 475 480

Asp Tyr Val Val Ile Gly Glu Asn Ala Gly Ser Lys Ala Thr Lys Ala 485 490 495

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cac His	cga Arg	gat Asp	cgt Arg 25	Tyr	tac Tyr	aac Asn	gaa Glu	cag Gln 30	cca Pro	gag Glu	atc Ile	cct Pro	gat Asp 35	gct Ala	gat Asp	211
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BGI-127CP - 215 -

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	cgt Arg															1795
	gac Asp															1843
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	gtg Val															1939
	tcg Ser 615															1987
	acc Thr															2035
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Leu Pro Gly Gly Arg Arg Pro Ile Gln Thr Ser Val Ile Pro Asp His 420 425 430

Lys Pro Gly Trp Val Lys Arg Gly Trp Glu Arg Ile Gly Glu Glu Val 435  $\phantom{000}$  440  $\phantom{000}$  445

Leu Ala Gly Arg Gln Ala Tyr Val Val Cys Pro Arg Ile Glu Gly Glu 450 455 460

Gly Gly Val Leu Glu Ile His Ala Tyr Leu Ser Glu Gln Val Tyr Pro 465 470 475 480

Gly Leu Asn Val Gly Met Leu His Gly Arg Met Asp Thr Asp Leu Lys 485 490 495

Asp Ser Val Met Gln Glu Phe Ala Gln Gly Glu Ile Asp Ile Leu Val 500 505 510

Ala Thr Val Ile Glu Val Gly Ile Asp Val Ala Asn Ala Thr Val 515 520 525

Met Leu Ile Arg Glu Ala Glu Arg Phe Gly Val Ser Gln Ile His Gln 530 535 540

Leu Arg Gly Arg Val Gly Arg Gly Gln His Asp Ser Leu Cys Leu 545 550 555 555

His Thr Thr Phe Asp Glu Asp Ser Pro Gln Gly Gln Arg Leu Ala Ala 565 570 575

Ile Ser Thr Thr Thr Asp Gly Phe Gln Leu Ser Glu Leu Asp Leu Gln 580 590

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Thr Lys Leu Arg His Leu Ser Phe Ile Ser Asp Gln Lys Ile Ile Glu 610 615 620

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880

903

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		40					45	,				50	O L J	- y -	Oru	

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65

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Tyr Ala Ser Gly Ile Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser 85 90 95

Ala Ile Leu Glu Ile Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro 100 105 110

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Pro Gly Pro His Asn Ala Phe His Pro Gly Val Gly Gly Ala Val Cys 165 170 175

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1 5

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490

1699

1740

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cca Pro	ctg Leu	agc Ser 200	cgg Arg	cga Arg	gaa Glu	gcc Ala	ctg Leu 205	aag Lys	aat Asn	att Ile	tago	cctc	ag (	gcatc	atctg	744
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Glu Arg Ala Phe Met Asp Ser Val Phe Gly Thr Phe Pro Asp Glu Ala 145 150 155 160

Thr Gln Val Ala Gly Ala Gly Asp Phe Phe Gly Ala Val Asp Tyr Glu 165 170 175

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Ser Ile Arg His Thr Arg Tyr His Gly Arg Val Glu Gly Pro Pro Lys

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gca ctg cgt Ala Leu Arg	tat cag cad Tyr Gln His 345	tca ggc ga Ser Gly Gl 35	g cgt gat gaa q u Arg Asp Glu ( 0	gag cta gca aag 1171 Glu Leu Ala Lys 355
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Lys Thr Gly Lys Lys Val Asp Val Pro Thr Asp Ala Glu Leu Glu Ala 165 170 175

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Asp Val Asp Val Tyr Phe Asp Arg Ser Gly Phe Val Asp Cys Val Arg 210 215 220

Ile Arg Ile Ser Arg Ser Ile Arg His Thr Arg Tyr His Gly Arg Val 225 230 235 240

Glu Gly Pro Pro Lys Thr Glu Ala Gly Val Arg Ser Leu Tyr Ile Tyr 245 250 255

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Tyr His Thr Phe Lys His Asn Trp Asp Arg Ala Arg Glu Ser Val His 290 295 300

Ser Lys Ala Thr Val His Ser Met Arg His Tyr Ser Gly Thr Lys Tyr 305 310 315 320

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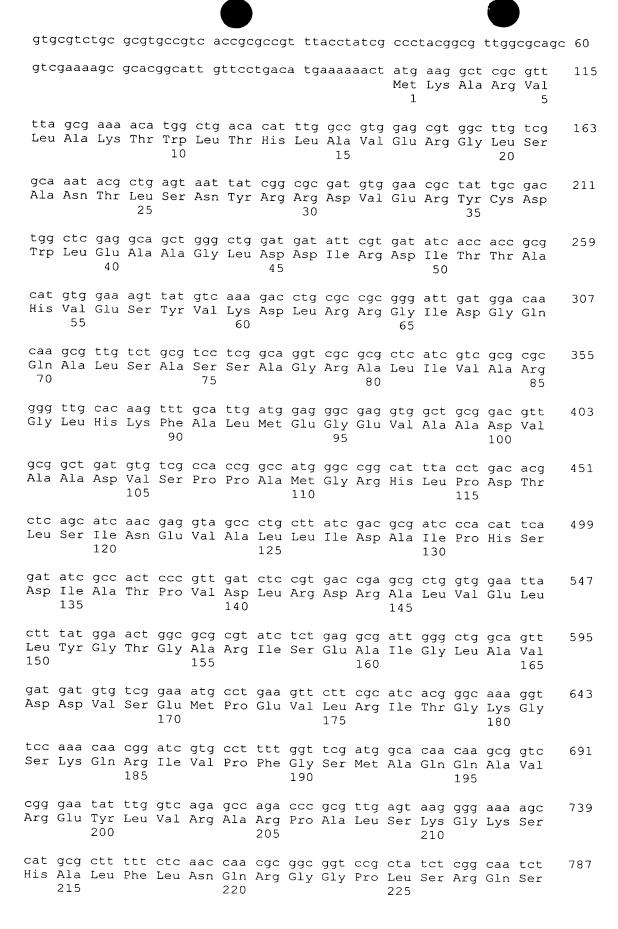
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							cac His									1027

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BGI-127CP

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His	Ser	Tyr	Trp	> A.	la 1 65	hr.	Ala	Glu	Gl	u L	eu 70	Leu	Thr	Glr	1 Т	rp	Ser 175	T	hr	

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120

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		acg Thr 195														624
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Val Met Pro Ala Trp Ala Met Leu Ser Met Gly Leu Ile Ala Leu Gly 50 55 60

Thr Ala Ser Pro Val Val Leu Gly Asp Asp Leu Trp Gly Phe Met Phe 65 70 75 80

Val Cys Trp Ser Ile Gly Thr Ala Val Gly Leu Val Ala Tyr Ser Leu 85 90 95

Tyr Ile Thr Ala Ile Leu Arg Ser Lys Ala Gly Thr Pro Thr Phe Ala 100 105 110

Trp Gly Leu Pro Leu Val Thr Pro Met Val Ala Ser Thr Ser Ala Ala 115 120 125

Gln Leu His Glu His Phe Glu Leu Pro Ala Met Leu Trp Val Ser Phe 130 135 140

Gly Leu Phe Leu Leu Thr Leu Ala Ser Ala Pro Ala Val Phe Thr Arg 145 150 155 160

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Ala Thr Pro Thr Ser Trp Ile Pro Leu Gly Met Val Gly Gln Ser Thr 180 185 190

Ala Ala Gln Leu Ile Gly Ala Ser Phe Gly Ser Lys Thr Ala Ile 195 200 205

Thr Met Gly Ile Ile Tyr Gly Ile Ile Met Gly Ile Phe Thr Ile Pro 210 215 220

Leu Gly Ala Ile Ala His Phe Val Phe Tyr Arg Ala Val Phe Lys Gly 235 235 240

Ala Thr Tyr Ser Pro Thr Trp Trp Ala Ser Thr Phe Pro Val Gly Thr 245 250 Leu Ser Leu Gly Ala His Phe Leu Ser Gln Ser Thr Gly Val Glu Trp 265 Phe Asn Tyr Phe Ser Leu Tyr Leu Ile Ala Leu Met Leu Phe His Val 280 Ile Val Ser Thr Ile Ala Gly Thr Ile Ala Val Met Arg Arg Ile Val Gly Lys Leu Lys Ser Gln Leu Ala 310 <210> 191 <211> 1017 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(994) <223> RXA00016 <400> 191 ctgaacggat ccgccaactt gaaaaggaaa atgcactcct ccgcgaagag cgtgacatcc 60 tgcggaaagc ggccaaatat ttcgcggaag agacgaactg gtg atc cgc ttc cga Val Ile Arg Phe Arg ttc gtt gat gac gct cga aag acc tac tcg gtt aag cgg ata tgt gac 163 Phe Val Asp Asp Ala Arg Lys Thr Tyr Ser Val Lys Arg Ile Cys Asp 10 gtg ttg aag ctc aat cgt tcc tca tat tac aaa tgg aaa agc acc gcc 211 Val Leu Lys Leu Asn Arg Ser Ser Tyr Tyr Lys Trp Lys Ser Thr Ala 25 ttc acg cgt gaa aaa cgc ctg ctc agc gac gct att ctt ggg gtc cag 259 Phe Thr Arg Glu Lys Arg Leu Leu Ser Asp Ala Ile Leu Gly Val Gln 40 gtc aag act gta ttc acc act cac agt ggc tgt tat ggg gcc aaa cga 307 Val Lys Thr Val Phe Thr Thr His Ser Gly Cys Tyr Gly Ala Lys Arg 55 atc gcg gct gaa ctc aaa gac cag atc ggc cat gac ctt gcg aac cac 355 Ile Ala Ala Glu Leu Lys Asp Gln Ile Gly His Asp Leu Ala Asn His 70 75 aag cgg gtt gcc cgg atc atg cga tcg ttg aag ctg ttc gga tac aca 403 Lys Arg Val Ala Arg Ile Met Arg Ser Leu Lys Leu Phe Gly Tyr Thr 90 aag aaa cgc aag gtc acc acc acc gtg ccg gac aaa acc aag aca gtg Lys Lys Arg Lys Val Thr Thr Thr Val Pro Asp Lys Thr Lys Thr Val 105

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Asp Leu Ala Asn His Lys Arg Val Ala Arg Ile Met Arg Ser Leu Lys 85 90 95

Leu Phe Gly Tyr Thr Lys Lys Arg Lys Val Thr Thr Thr Val Pro Asp 100 105 110

Lys Thr Lys Thr Val Phe Pro Asp Leu Val Gly Arg Lys Phe Thr Ala 115 120 125

Asp Lys Pro Asn Gln Leu Tyr Val Gly Asp Ile Thr Tyr Leu Pro Ile 130 140

Gln Asp Gly Ser Asn Met Tyr Leu Ala Thr Val Ile Asp Cys Tyr Ser 145 150 155 160

Arg Arg Leu Val Gly Phe Ser Ile Ala Asp His Met Arg Thr Ser Leu 165 170 175

Val Gln Asp Ala Leu Leu Met Ala Lys Asp Gln Arg Gly Asn Leu Lys 180 185 190

Gly Ala Ile Phe His Ser Asp His Gly Ser Val Tyr Thr Ser His Ala 195 200 205

Phe Gln Glu Thr Cys Lys Lys Leu Gly Ile Arg Gln Ser Met Gly Ser 210 215 220

Ile Gly Thr Ser Ala Asp Asn Ala Leu Ala Glu Ser Phe Asn Ala Ala 225 230 235 240

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acc ttg ctg Thr Leu Leu	gaa tcc Glu Ser 105	cgc gaa Arg Glu	ggt cad Gly His 110	Leu Ala	gca cgc A Ala Arg	aca gcc Thr Ala 115	tgc Cys	451
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Pro Thr Val Glu His Arg

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Met Asp Glu Leu Ala

1 5

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ttc aat atc ggt gca tcc aac gga cct gtc gag gcc atc aac ggc aga
Phe Asn Ile Gly Ala Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg
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30
31

ctt gag cac ctg cgc ggg atc acc ttg ggg ttc agg aac ctc aac cac 259 Leu Glu His Leu Arg Gly Ile Thr Leu Gly Phe Arg Asn Leu Asn His

tac atc ttg cgg tgc ttg atc caa gcc gga caa ctg cag agg aag at Tyr Ile Leu Arg Cys Leu Ile Gln Ala Gly Gln Leu Gln Arg Lys I:	tc 307 le
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Ala Ile Asn Gly Arg Leu Glu His Leu Arg Gly Ile Thr Leu Gly Ph 35 40 45	ıe
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ctc gat gct tgc cga cag ctc att tac aac gac ccg cgc cac ctt ga Leu Asp Ala Cys Arg Gln Leu Ile Tyr Asn Asp Pro Arg His Leu Gl 25 30 35	a 211 u
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                                             Met Ser Ile Ala Ala
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                                                                    163
Thr Ala Lys Ala Leu Gly Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala
                 10
                                      15
cta gat atg tgc cac gaa ctc atc tac tac gac ccc acc cac cta gaa
                                                                    211
Leu Asp Met Cys His Glu Leu Ile Tyr Tyr Asp Pro Thr His Leu Glu
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att gtg cac gtt att ggc gtc gat gag cac aaa tgatctcata accgattaaa 264
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Pro Thr His Leu Glu Ile Val His Val Ile Gly Val Asp Glu His Lys 35 40 45

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gat Asp	gac Asp	ccg Pro	ttg Leu	tat Tyr 90	aag Lys	aac Asn	cgg Arg	aaa Lys	acc Thr 95	ttg Leu	ctg Leu	acc Thr	acg Thr	caa Gln 100	aaa Lys	403
tgg Trp	ttg Leu	agt Ser	aag Lys 105	aaa Lys	aaģ Lys	caa Gln	agc Ser	gtc Val 110	ttg Leu	atg Met	agt Ser	tgt Cys	tta Leu 115	gct Ala	ttg Leu	451
ata Ile	aag Lys	act Thr 120	acg Thr	cgg Arg	cac His	tgc Cys	aac Asn 125	tgat	gtgg	gca <u>c</u>	gcgt	atca	aa go	gc		498

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Ile Thr Ala Glu Leu Asn Asp Asp Pro Gly Ser Thr Pro Val Asn His

Lys Arg Val Ala Arg Ile Met Ala Ser Leu Lys Leu Phe Gly Phe Thr

Lys Lys Arg Arg Val Ile Thr Thr Val Ser Asp Lys Lys Pro Val

Phe Pro Asp Leu Val Lys Arg His Phe Asn Ala Leu Ala Ala Asn Glu 105

Val Tyr Val Gly Asp Ile Thr Tyr Leu Pro Ile Ala Asp Gly Thr Asn 115

Met Tyr Leu Ala Thr Val Ile Asp Cys Tyr Ser Arg Arg Leu Val Gly 135

Phe Ala Ile Ala Asp His Met Arg Thr Ser Leu Val Gln Glu Ala Leu 155 150

Leu Met Ala Lys Ser Gln Arg Gly Ser Leu Lys Gly Ala Val Phe His 170

Ser Asp His Gly Ser Val Tyr Thr Ser Gln Ala Phe Gln Asp Thr Cys 185

Lys Lys Leu Gly Val Arg Gln Ser Met Gly Ala Val Gly Thr Ser Ala 200

Asp Asn Ser Leu Ala Glu Ser Phe Asn Ala Ala Leu Lys Arg Glu Val 210

Leu Gln Asp Ser Lys Thr Phe Ala Asn Gln Leu Val Cys Arg Arg Glu 235 230

Val Phe Arg Trp Cys Thr Arg Tyr Ser Thr Asn Arg Arg His Ser Trp 250



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tat tcc gag gag ttc aaa cgc gac gcc gtt gct ttg tac gag aac tcc 163
Tyr Ser Glu Glu Phe Lys Arg Asp Ala Val Ala Leu Tyr Glu Asn Ser
10 15 20

gac ggg gcc tca ctc caa cag atc gcc aac gat ctc ggc atc aac cga 211
Asp Gly Ala Ser Leu Gln Gln Ile Ala Asn Asp Leu Gly Ile Asn Arg
25 30 35

gta acc ctg aaa aac tgg atc atc aaa tac gga tcc aac cac aac gta 259 Val Thr Leu Lys Asn Trp Ile Ile Lys Tyr Gly Ser Asn His Asn Val

caa ggg aca acc cca tct gcg gca gtc tct gaa gct gaa caa atc cgg 307 Gln Gly Thr Thr Pro Ser Ala Ala Val Ser Glu Ala Glu Gln Ile Arg 55 60 65

cag ctg aag aag gaa aac gcg cta caa cgc gca aga acg cga cat cct 355 Gln Leu Lys Lys Glu Asn Ala Leu Gln Arg Ala Arg Thr Arg His Pro 70 75 80 85

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Cys Gly Ala Cys Gly Val

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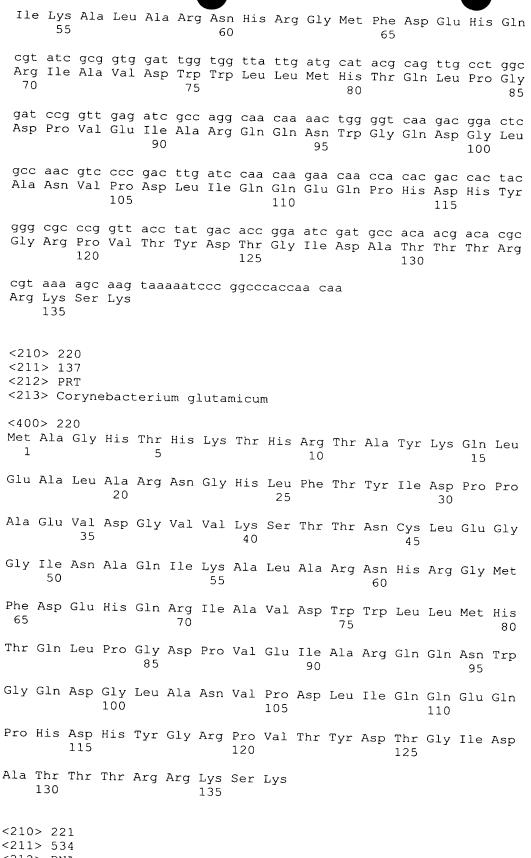
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534



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                                              Met Ala Gly His Thr
 cac aaa acc cac cgg act gct tat aag cag ttg gaa gcc ttg gcc cgc
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 His Lys Thr His Arg Thr Ala Tyr Lys Gln Leu Glu Ala Leu Ala Arg
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                                       15
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Asn Gly His Leu Phe Thr Tyr Ile Asp Pro Pro Ala Glu Val Asp Gly
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gtg gtg aaa tca aca acg aac tgt ttg gaa ggt ggt atc aac gct cag
                                                                    259
Val Val Lys Ser Thr Thr Asn Cys Leu Glu Gly Gly Ile Asn Ala Gln
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att aaa gcg ttg gcg aga aac cat cgg ggg atg ttt gat gaa cat caa
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Ile Lys Ala Leu Ala Arg Asn His Arg Gly Met Phe Asp Glu His Gln
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Arg Ile Ala Val Asp Trp Trp Leu Leu Met His Thr Gln Leu Pro Gly
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                                                                    403
Asp Pro Asp Glu Ile Ala Arg Gln Gln Asn Trp Gly Gln Asp Gly Leu
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                                      95
gcc aac gtc ccc gac ttg atc caa caa gaa caa cca cac gac cac tac
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Ala Asn Val Pro Asp Leu Ile Gln Gln Glu Gln Pro His Asp His Tyr
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80

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	atc Ile															451
	aag Lys															499
	tac Tyr 135															547
	ctg Leu		_	_						_			_			595
	ttg Leu			_	_		-							_		643
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Glu His Arg Gln Val Lys Tyr Leu Asn Asn Val Ile Glu Gly Asp His 130 135 140

Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly Ala Phe Lys Asn Arg 145 150 155 160

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Thr Arg

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Thr	Thr	Ile	Tyr	Arg	Trp	Val	Gln	Lvs	Tvr	Ála	Leu	Glu	Leu	Asp	Lvs	
1				5	-			-	10				200	15	цуз	

cag act cgc tgg tac cgg cag gtt cct gac tgg cag gcc agt tcc tgg 96 Gln Thr Arg Trp Tyr Arg Gln Val Pro Asp Trp Gln Ala Ser Ser Trp 20 25

cgg gtg gat gag acc tat atc cgg gtc ggc ggc acg tgg tgc tat ctc  $^{144}$  Arg Val Asp Glu Thr Tyr Ile Arg Val Gly Gly Thr Trp Cys Tyr Leu  $^{35}$ 

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Tyr Arg Ala Ile Thr Ala Gly Gly Gln Thr Leu Glu Phe Tyr Leu Ser
50 55 60

cca aaa cgg aat gtg gct gcg gcc aag cgt ttc ctg gcc aag acg ctg
Pro Lys Arg Asn Val Ala Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu
65 70 75

cga tcg aat acg aca gcc ggg tcc ccg cgg gtc atc aac acc gac aag 288
Arg Ser Asn Thr Thr Ala Gly Ser Pro Arg Val Ile Asn Thr Asp Lys
85 90 95

gca cca gct ctg gcc aag gca ata tcc gag ctg aag gcg gag gga atc 336 Ala Pro Ala Leu Ala Lys Ala Ile Ser Glu Leu Lys Ala Glu Gly Ile 100 105

tgc cct cag acg gtg gag cac cgg cag gtg aaa tac ctc aac aac gtt Cys Pro Gln Thr Val Glu His Arg Gln Val Lys Tyr Leu Asn Asn Val 115

atc gag gga gat cat ggc cga ctt aaa aga atc ctg ggg ccg aag gga 432 Ile Glu Gly Asp His Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly

140 gcg ttc aaa aac cga att tcc gcc tac cgg acg ttg aaa ggg atg gaa 480 Ala Phe Lys Asn Arg Ile Ser Ala Tyr Arg Thr Leu Lys Gly Met Glu gcg atg cat tca tta cgg aaa ggc cag ggc acg atg ttt gac ctc acg Ala Met His Ser Leu Arg Lys Gly Gln Gly Thr Met Phe Asp Leu Thr

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Arg Val Asp Glu Thr Tyr Ile Arg Val Gly Gly Thr Trp Cys Tyr Leu 35

Tyr Arg Ala Ile Thr Ala Gly Gly Gln Thr Leu Glu Phe Tyr Leu Ser

Pro Lys Arg Asn Val Ala Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu

Arg Ser Asn Thr Thr Ala Gly Ser Pro Arg Val Ile Asn Thr Asp Lys

Ala Pro Ala Leu Ala Lys Ala Ile Ser Glu Leu Lys Ala Glu Gly Ile 100

Cys Pro Gln Thr Val Glu His Arg Gln Val Lys Tyr Leu Asn Asn Val

Ile Glu Gly Asp His Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly

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<213> Corynebacterium glutamicum

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Ile Asn Gln His Glu Gly Ser Leu Arg Lys Leu Phe Asp Lys Phe Leu 35 40 45

Ala Asn Asp Ala Glu Val Leu Val Val Val Asp Gln Pro Asn Asn Ile 50 55 60

Gly Arg Leu Thr Val Ala Val Ala Gln Ala Met Gly Ala Asp Val Arg 65 70 75 80

Tyr Leu Pro Gly Leu Ala Met Arg Gln Leu Ser Arg Ile His Val Gly
85 90 95

Asn Ser Lys Thr Asp Val Arg Asp Ala Tyr Val Ile Ala His Ala Gly 100 105 110

Leu Asn Leu Pro Asp Ala Leu Arg Ser Val Asp Arg Val Glu Glu Val
115 120 125

Phe Leu Gln Leu Lys Val Leu Asn Gly Ile Asp Glu Asp Leu Ala Arg 130 135 140

Ala Tyr Thr Arg Leu Ile Asn Gln Met Gln Ser Ala Leu Val Gly Thr 145 150 155 160

Tyr Pro Ala Phe Glu His Val Leu Arg Gly Gln Met Ile His Arg Lys 165 170 175

Trp Ile Leu His Leu Leu Ala Lys Tyr Gly Gly Pro Thr Lys Ile Arg 180 185 190

Arg Val Gly Lys Ala Arg Leu Ala Ala Phe Ala Arg Gly His Arg Ala 195 200 205

Arg Asn Pro Glu Pro Val Ile Asp Ala Met Leu Ala Ala Ile His Gly 210 215 220

Gln Thr Val Ser Ile Ala Gly Ala Glu Tyr Ala Glu Leu Gly Val Ala 225 230 235 240

Met Ser Ala Lys Asp Ala Leu Ala Lys Leu Glu His Arg Lys Glu Ile 245 250 255

Glu Gly Gln Val Leu Glu Leu Ile Gln Asp Ile Pro Gln Thr Glu Ile 260 265 270

Leu Leu Ser Met Pro Gly Ile Gly Pro Arg Ser Ala Ala Gln Ile Leu 275 280 285

Met Thr Val Gly Asp Met Ser Asp Phe Pro Asp Ala Ala His Leu Ala 290 295 300

Ser Tyr Ala Gly Leu Ser Pro Gln Thr Asn Gln Ser Gly Thr Ser Ile 305 310 315 320

Met Ser Asn Ser Pro Asn Arg Ala Gly Asn Lys Lys Leu Lys Asn Ala Leu Trp Gln Ser Ser Phe Ala Ser Ile Arg Phe His Glu Arg Ser Arg 345 350 Gln Phe Tyr Glu Arg Lys Arg Asn Glu Gly Lys Arg His Asn Ala Ala 360 Val Val Ala Leu Ala Arg Arg Arg Leu Asn Val Leu Phe Ala Met Met 375 Arg Ser Gly Glu Leu Tyr Arg Asp Ile Pro Thr Ala Gln Glu Ala Ala 390 395 Ala Ala <210> 229 <211> 504 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(481) <223> RXA01953 <400> 229 gcatatcagc agcagtatgg attagcagca gcgtaagaag aaaaatcaat caagctgtct 60 caaaaacttg acgagcgcaa cctgggggat ctaccagcgg atg atc gcg gcc tac 115 Met Ile Ala Ala Tyr ege gag aag gae ega tee ete gge ege geg geg atg gag geg ete ate 163 Arg Glu Lys Asp Arg Ser Leu Gly Arg Ala Ala Met Glu Ala Leu Ile 10 gac gcc gtc agc caa gac gtc ccc gcc ggg ctg gac gag ttg cgc aag 211 Asp Ala Val Ser Gln Asp Val Pro Ala Gly Leu Asp Glu Leu Arg Lys ctc ggt cgg acc ctg aag gct cgc gcc acc gac gtg ctg gcc tac ttc 259 Leu Gly Arg Thr Leu Lys Ala Arg Ala Thr Asp Val Leu Ala Tyr Phe gag egg eet gge aee age aat gge eee aea gag geg ate aae gga ege 307 Glu Arg Pro Gly Thr Ser Asn Gly Pro Thr Glu Ala Ile Asn Gly Arg 55 60 ctg gag cac ctg cgc ggc tcg gcc ctg ggc ttc cgc aac ctg acc aac 355 Leu Glu His Leu Arg Gly Ser Ala Leu Gly Phe Arg Asn Leu Thr Asn 70 75 tac atc gcc aga tcc ctg ctc gag ttc cgg cgg att cag acc tca act 403 Tyr Ile Ala Arg Ser Leu Leu Glu Phe Arg Arg Ile Gln Thr Ser Thr

aca ccc tca tct gtg aag agc cgc ttt aga cat ccc tca tcg tca cgg

451

Thr Pro Ser Ser Val Lys Ser Arg Phe Arg His Pro Ser Ser Ser Arg 110 acc act atg aac gat gtc ccg act cac cta tgaacgatgt cctgaaccta 501 Thr Thr Met Asn Asp Val Pro Thr His Leu 125 cac 504 <210> 230 <211> 127 <212> PRT <213> Corynebacterium glutamicum <400> 230 Met Ile Ala Ala Tyr Arg Glu Lys Asp Arg Ser Leu Gly Arg Ala Ala Met Glu Ala Leu Ile Asp Ala Val Ser Gln Asp Val Pro Ala Gly Leu 20 Asp Glu Leu Arg Lys Leu Gly Arg Thr Leu Lys Ala Arg Ala Thr Asp Val Leu Ala Tyr Phe Glu Arg Pro Gly Thr Ser Asn Gly Pro Thr Glu 50 Ala Ile Asn Gly Arg Leu Glu His Leu Arg Gly Ser Ala Leu Gly Phe Arg Asn Leu Thr Asn Tyr Ile Ala Arg Ser Leu Leu Glu Phe Arg Arg 85 Ile Gln Thr Ser Thr Thr Pro Ser Ser Val Lys Ser Arg Phe Arg His 100 105 Pro Ser Ser Ser Arg Thr Thr Met Asn Asp Val Pro Thr His Leu 115 120 <210> 231 <211> 831 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(808) <223> RXA01998 <400> 231 aaccatcatc ttggagttca gggtcacctg caggataacc taaaacggtg ctgttgcaaa 60 gttggggcag taggaagacc ggcgtggaat aatcaggtcc atg ggc atc ttc tcc Met Gly Ile Phe Ser

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Gly Arg Gln Phe Pro Arg Glu Ile Ile Leu Trp Ala Val Arg Trp Tyr

15

10

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tat gc Tyr Ala 5	4 110	gag ct Glu Le	g gat u Asp	aag Lys 60	aag Lys	acc Thr	cgg Arg	tgg Trp	tat Tyr 65	cgg Arg	caa Gln	gtt Val	cct Pro	307
gac tgg Asp Trp 70	g cag p Gln 2	gcc ag Ala Ar	g tcc g Ser 75	тrр	cgg Arg	gtg Val	gat Asp	gag Glu 80	acc Thr	tat Tyr	atc Ile	cgg Arg	gtc Val 85	355
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acc cto Thr Leu		tc tac Phe Tyr .05	ctc Leu	tcc Ser	ccg Pro	aag Lys 110	aga Arg	aac Asn	gtc Val	gcg Ala	gcg Ala 115	gcg Ala	aag Lys	451
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gtg aaa Val Lys	tac c Tyr L	tc aac eu Asn 170	aac Asn	gtc . Val	att ( Ile (	JLU (	ggc Gly 175	gac Asp	cat ( His (	ggt Gly	cgg Arg	tta Leu 180	aag Lys	643
cgg atc Arg Ile	Leu G.	gg ccg ly Pro 85	aaa Lys	ggc ( Gly )	Ala I	tc a Phe 1	aaa Lys .	aac Asn	cga a Arg :	Thr :	tct Ser 195	gcc Ala	tac Tyr	691
cgg acg Arg Thr	ttg aa Leu Ly 200	aa ggg ys Gly	atg Met	GIU F	gcg a Ala N 205	atg d Met H	cac d	tca : Ser 1	Leu A	egg a Arg 1 210	aag Lys	Gly ggg	cag Gln	739
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<213> Corynebacterium glutamicum

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35 40 45

Arg Trp Val Gln Lys Tyr Ala Pro Glu Leu Asp Lys Lys Thr Arg Trp 50 55 60

Tyr Arg Gln Val Pro Asp Trp Gln Ala Arg Ser Trp Arg Val Asp Glu 65 70 75 80

Thr Tyr Ile Arg Val Gly Gly Lys Trp Cys Tyr Leu Tyr Arg Ala Ile 85 90 95

Thr Ala Gly Ser Gln Thr Leu Asp Phe Tyr Leu Ser Pro Lys Arg Asn 100 105 110

Val Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu Arg Ser Asn Lys 115 120 125

Ser Ala Gly Tyr Pro Arg Val Ile Ser Thr Asp Lys Ala Pro Ser Leu 130 135 140

Ala Arg Ala Ile Ser Glu Leu Lys Ala Glu Gly Val Cys Pro Ser Thr 145 150 155 160

Val Glu His Arg Arg Val Lys Tyr Leu Asn Asn Val Ile Glu Gly Asp 165 170 175

His Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly Ala Phe Lys Asn 180 185 190

Arg Thr Ser Ala Tyr Arg Thr Leu Lys Gly Met Glu Ala Met His Ser 195 200 205

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ccc o	gaa ( Glu (	ggg . Gly (	tgc ( Cys (	gaa Glu ' 10	gtg ( Val (	ggc ( Gly )	att d Ile <i>l</i>	egt Arg .	aga a Arg 1	aca a Thr I	atc ( [le ]	cca « Pro (	gag Glu	gaa Glu 20	agc Ser	163

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gat : Asp :	ttt Phe	ttc Phe	Pro	aag Lys 490	ggc Gly	act Thr	aat Asn	Phe .	gct Ala 495	aaa Lys	gta Val	agt Ser	gac Asp	gaa Glu 500	gaa Glu	1603
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Arg Gly Gly Asn Ala Phe Asp Thr Ala Glu Lys Leu Glu Ile Ala Ala 65 70 75 80

Ser Met Leu Glu Lys Gly Cys Leu Pro Arg Glu Ile Gly Glu Tyr Val 85 90 95

Gly Met Thr Arg Ala Asn Ile Ser Leu Trp Arg Lys Gln Gly Pro Asp 100 105 110

Lys Leu Arg Gln Arg Ala Ala Thr Leu Arg Thr Gly Lys Arg Ala Ala 115 120 125

Glu Phe Ile His Ala Pro Val Met Gly Pro Tyr Tyr Gly Pro Arg Thr 130 135 140

Leu His Gln Val Leu Arg Glu Asp Tyr Thr Thr Leu Phe Asp Glu Leu 145 150 155 160

Ser Ala Leu Gly Leu Pro Ala Gln Val Cys Gly Ala Leu Leu His Leu 165 170 175

Ala Pro Pro Pro Ser Leu Arg Phe Ser Tyr Met Ser Cys Val Val Pro 180 185 190

Leu Phe Ala Asp Glu Ile Lys Val Val Gly Gln Gly Thr Arg Leu Ser 195 200 205

Leu Glu Glu Lys Met Met Ile Gln Arg Phe His Asp Thr Gly Val Ser 210 215 220

Ala Ala Glu Ile Gly Arg Arg Leu Gly Arg Cys Arg Gln Thr Ile Ser

225

230 235 240 Arg Glu Leu Arg Arg Gly Gln Asp Asp Asp Gly Arg Tyr Arg Ala Arg 250 Asp Ser Tyr Glu Gly Ala Ile Arg Lys Leu Ala Arg Pro Lys Thr Pro Lys Leu Asp Ala Asn Arg Arg Leu Arg Ala Val Val Glu Ala Leu Asn Asn Lys Leu Ser Pro Glu Gln Ile Ser Gly Leu Leu Ala Thr Glu His Ala Asn Asp Ser Ser Met Gln Ile Ser His Glu Thr Ile Tyr Gln 315 Ala Leu Tyr Val Gln Gly Lys Gly Ala Leu Arg Asp Glu Leu Lys Val Glu Lys Phe Leu Arg Thr Gly Arg Lys Gly Arg Lys Pro Gln Ser Lys Leu Pro Ser Arg Gly Lys Pro Trp Val Glu Gly Ala Leu Ile Ser Gln Arg Pro Ala Glu Val Ala Asp Arg Ala Val Pro Gly His Trp Glu Gly Asp Leu Val Ile Gly Gly Glu Asn Gln Ala Thr Ala Leu Val Thr Leu Val Glu Arg Thr Ser Arg Leu Thr Leu Ile Lys Arg Leu Gly Val Asn His Glu Ala Ser Thr Val Thr Asp Ala Leu Val Glu Met Met Gly Asp 425 Leu Pro Gln Ala Leu Arg Arg Ser Leu Thr Trp Asp Gln Gly Val Glu Met Ala Glu His Ala Arg Phe Ser Val Val Thr Lys Cys Pro Val Phe Phe Cys Asp Pro His Ser Pro Trp Gln Arg Gly Ser Asn Glu Asn Thr Asn Gly Leu Val Arg Asp Phe Phe Pro Lys Gly Thr Asn Phe Ala Lys Val Ser Asp Glu Glu Val Gln Arg Ala Gln Asp Leu Leu Asn Tyr Arg Pro Arg Lys Met His Gly Phe Lys Ser Ala Thr Gln Val Tyr Glu Lys 525 Ile Val Val Gly Ala Ser Thr Asp

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gtt Val	gcg Ala	tat Tyr	gcg Ala	ttg Leu 90	gtt Val	ttt Phe	gct Ala	gcg Ala	gtt Val 95	cgt Arg	gag Glu	ttg Leu	ttt Phe	gaa Glu 100	gag Glu	403

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Lys 65	Glu	Val	Trp	Arg	Gly 70	Pro	Ser	Ala	Glu	Glu 75	Trp	Gly	Val	Arg	Leu 80	
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195

200 205

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Gln Phe Lys Thr Val Glu Glu Leu Leu Glu Tyr Ser Ala Gln Val Asp 225 235 235 240

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Leu Ile Leu Pro Val

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ccc cag gac ctt gat gtt cat gtt att tgt gac aac tac gcc acg cat  $\,$  259 Pro Gln Asp Leu Asp Val His Val Ile Cys Asp Asn Tyr Ala Thr His  $\,$  40  $\,$  45  $\,$  50

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Asn Tyr Ala Thr His Lys His Pro Thr Ile Asn Thr Trp Leu Val Lys 50 55 60

His Pro Arg Phe His Met His Phe Thr Pro Thr Tyr Ser Ser Trp Ile 65 70 75 80

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Arg Ser Asp His Arg Ser Val Gln Ala Leu Glu Lys Asp Leu Arg Asn 100 105 110

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_				_				_	-	-	gat Asp 65	-	_			307
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Asp Val Cys Leu Gly Thr Val Leu Arg Ala Trp Glu Ala Leu Ser Leu 65 70 75 80

Arg Trp Val Asp Val Val Leu Asp Glu Glu His Pro Arg Ile Phe Ile 85 90 95

Arg Gly Thr Ile Val Tyr Asn Lys Glu Lys Gly Asn His Arg Gln Asp 100 105 110

Lys Thr Lys Thr Thr Ser Ser Arg Arg Val Ile Gln Leu Pro Glu Ile 115 120 125

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Leu Arg Leu Ile Lys Leu Ser Lys Ser Thr Ala Tyr Tyr Arg Asn Lys 35 40 45

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Pro Thr Ala Pro Gly Val Glu Pro Thr Pro Glu Pro Trp Gln Gly Lys
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Glu Pro Ala Val Ser Ser Val Arg Gln Ala Leu Ala Glu His Glu Arg 85 90 95

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Gly Val Phe Asn Met Leu Phe Asn Lys Gly Ile Tyr Arg Ala Ser Leu 115 120 125

Arg Thr Trp Trp Arg Val Ala Lys Gln His Lys Leu Leu His Lys Asp 130 135 140

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Lys Pro Arg Leu Glu Ala Thr Gln Pro Gly Gln Val Val Cys Trp Asp 165 170 175

Val Thr Phe Leu Pro Ser Leu Val Arg Gly Lys Thr Tyr Ala Leu His 180 185 190

Leu Ala Ile Asp Leu Phe Ser Arg Lys Ile Val Gly Ala Lys Val Ala 195 200 205

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Ala Asp Asn Pro Gly Val Val Thr Val His Ser Asp Asn Gly Ser Ala 225 230 235 240

Met Thr Ser Thr Arg Val Arg Arg Leu Leu Ala Asp His Gly Val Ala 245 250 255

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Ser Val Phe His Thr Leu Lys Tyr Arg Pro Phe Tyr Pro Lys Val Phe 275 280 285

Ala Ser Met Asp Gln Ala Arg Val Trp Val Glu Glu Phe Val Val Tyr

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Lys	Pro	Arg	Leu	Glu 165	Ala	Thr	Gln	Pro	Gly 170	Gln	Val	Val	Cys	Trp 175	Asp	
Val	Thr	Phe	Leu 180	Pro	Ser	Leu	Val	Arg 185	Gly	Lys	Thr	Tyr	Ala 190	Leu	His	
Leu	Ala	Ile 195	Asp	Leu	Phe	Ser	Arg 200	Lys	Ile	Val	Gly	Ala 205	Lys	Val	Ala	
Pro	Thr	Glu	Asn	Thr	Ser	Thr	Ala	Val	Glu	Leu	Leu	Thr	Gln	Val	Leu	

210 215 220 Ala Asp Asn Pro Gly Val Val Thr Val His Ser Asp Asn Gly Ser Ala 235 Met Thr Ser Thr Arg Val Arg Arg Leu Leu Ala Asp His Gly Val Ala Leu Ser Leu Ile Arg Pro Arg Val Ser Asp Asp Asn Ala Phe Val Glu Ser Val Phe His Thr Leu Lys Tyr Arg Pro Phe Tyr Pro Lys Val Phe 280 285 Ala Ser Met Asp Gln Ala Arg Val Trp Val Glu Glu Phe Val Val Tyr Tyr Asn Thr Val His Pro His Ser Gly Val Ala Gly His Thr Pro Gln 305 310 315 Ser Val Phe Asp Gly Ser Trp Arg Ala Ala His Arg Leu Arg Val Gln 325 330 Ala Leu Asp Ala His Tyr Arg Gln Phe Pro Gln Arg Tyr Val Gly Arg 340 345 350 Pro Val Val Gln Glu Val Ala Gly Val Val Arg Leu Asn Gly Ala Arg 360 Asp Asp Gly Ser Val Gln Glu Arg Val Gly Gly Val Ala Ser Leu Leu 375 380 Ser Ala 385 <210> 255 <211> 1065 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1042) <223> RXN03049 <400> 255 accagggtgc acgttccctg cacttcatcg ccatggtgtt gatgacgggc tttgtcatca 60 tgcacgtcgg cctggttttt tggtccatgg cgactacaac atg gtc cac atg gtc 115 Met Val His Met Val ttc ggc gat atg aac act gac cgt gcg gcg cag gcc tac atc atc gtg 163 Phe Gly Asp Met Asn Thr Asp Arg Ala Ala Gln Ala Tyr Ile Ile Val atc acc acc atc gtc atg gtg gtg ttg ttc tgg atc gtg ctc aga tat

Ile Thr Thr Ile Val Met Val Val Leu Phe Trp Ile Val Leu Arg Tyr

30

25

211

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acg Thr	gag Glu 55	Ile	gga Gly	cgc Arg	aaa Lys	atc Ile 60	ttc Phe	ctc Leu	aac Asn	cgg Arg	ctg Leu 65	cgt Arg	ccc Pro	cgg Arg	atg Met	307
agc Ser 70	Arg	cag Gln	aac Asn	acc Thr	tac Tyr 75	acg Thr	gac Asp	aag Lys	gac Asp	atc Ile 80	tcg Ser	cag Gln	ttc Phe	cac His	tgg Trp 85	355
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gcc Ala	cgc Arg	gac Asp	aac Asn 105	gag Glu	tgg Trp	gag Glu	gga Gly	tac Tyr 110	acc Thr	atc Ile	acc Thr	ctc Leu	ggc Gly 115	gac Asp	gat Asp	451
ccc Pro	aac Asn	ggc Gly 120	acc Thr	gag Glu	aaa Lys	acc Thr	atc Ile 125	acc Thr	ctc Leu	gac Asp	gat Asp	ctg Leu 130	cgg Arg	gag Glu	ctg Leu	499
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aag Lys	atc Ile	atc Ile 200	gat Asp	ttc Phe	gat Asp	ctg Leu	ttc Phe 205	gca Ala	ccg Pro	aac Asn	agt Ser	ccc Pro 210	tcg Ser	atc Ile	gaa Glu	739
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cgg	усс	gat	ctc	tat	ycg	att	cga .	agg	cat	ckc	cac	cgg	gga	act	gac	979

Arg Xaa Asp Leu Tyr Xaa Ile Arg Arg His Xaa His Arg Gly Thr Asp 280 285 285

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<400> 256

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Phe Thr Ala Ser Ile Thr Glu Ile Gly Arg Lys Ile Phe Leu Asn Arg 50 55 60

Leu Arg Pro Arg Met Ser Arg Gln Asn Thr Tyr Thr Asp Lys Asp Ile
65 70 75 80

Ser Gln Phe His Trp Thr Asn Gly Leu Pro Pro Thr Asp Asp Glu Ser 85 90 95

Pro Glu Trp Ile Ala Ala Arg Asp Asn Glu Trp Glu Gly Tyr Thr Ile 100 105 110

Thr Leu Gly Asp Asp Pro Asn Gly Thr Glu Lys Thr Ile Thr Leu Asp 115 120 125

Asp Leu Arg Glu Leu Pro Gln Thr Ser Tyr Val Ala Val His Thr Cys 130 135 140

Met Gln Gly Trp Ser Ala Thr Ala Arg Trp Thr Gly Val Arg Leu Arg 145 150 155 160

Asp Val Leu Cys His Asp Leu Val His Thr Leu Asp Leu His His Arg 165 170 175

His Ser Pro Arg Leu Leu Thr Ile Glu Ile Ile Pro Lys Pro Leu Pro 180 185 190

Pro Glu Thr Arg Cys Lys Ile Ile Asp Phe Asp Leu Phe Ala Pro Asn 195 200 205

Ser Pro Ser Ile Glu Glu Phe Cys Ser Arg Leu Lys Ile Ser Arg Arg 210 215 220

Ser Phe Tyr Asn Ile Arg Asn Arg Tyr Gln Gln Asp Ala Ser Ala Ala

225 230 235 240 Leu His Pro Arg Ser Ser Ala Gln Ile Thr Ser Arg Arg Thr Tyr Asp 250 Glu Ser Ile Thr Ser Ile Leu Leu Ala Ile Arg Ala Pro Pro Glu Ser 265 Pro Arg Met Gly Xaa Arg Xaa Asp Leu Tyr Xaa Ile Arg Arg His Xaa 280 His Arg Gly Thr Asp Cys Thr Asp Ser Ile Arg Leu Asn Tyr Arg Leu 295 300 Leu Val Thr Arg Cys Arg Ser Ser Arg Lys 310 <210> 257 <211> 951 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(928) <223> RXN03070 <400> 257 gtggataaaa gggaaaacat aggggtcatg aaatagaaca agcacgaggc ctggtaaata 60 cgaattcgac caagaaaacg taaacacccc aggagtactc gtg cct gcc ctt cca Val Pro Ala Leu Pro tca tct atc atc gac ccc ctc tgg cgc cag ttc tcc gcc tta atc cca 163 Ser Ser Ile Ile Asp Pro Leu Trp Arg Gln Phe Ser Ala Leu Ile Pro ccg gtt atc atc acc cac cca cta ggg tgc cac cgt gca cgc att gct 211 Pro Val Ile Ile Thr His Pro Leu Gly Cys His Arg Ala Arg Ile Ala gac egg ate ate gte gac aaa ete ate gea gtg ett gte ete ggt gte 259 Asp Arg Ile Ile Val Asp Lys Leu Ile Ala Val Leu Val Leu Gly Val 4.5 tcc tat atc aag att tcc gat tcc acc tgc tca gcc acc acg ata cgc 307 Ser Tyr Ile Lys Ile Ser Asp Ser Thr Cys Ser Ala Thr Thr Ile Arg acc cgc cga gac gag tgg atc act gcc ggg att ttc aag aat tta gaa Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile Phe Lys Asn Leu Glu 75 cag atc tgt ctg gag tcc tac gac cgt ttc atc ggg tta gac cta gaa 403 Gln Ile Cys Leu Glu Ser Tyr Asp Arg Phe Ile Gly Leu Asp Leu Glu aac tta aat gtt gat ggc tgc att gtt aaa gct ccc tgc ggc gga gag Asn Leu Asn Val Asp Gly Cys Ile Val Lys Ala Pro Cys Gly Gly Glu

105 110 115 gta gcc ggc aga ttc ccg gtt gac cgg gaa aaa ggc acc aaa cgc tcg 499 Val Ala Gly Arg Phe Pro Val Asp Arg Glu Lys Gly Thr Lys Arg Ser tta atg gtc gat gga cat gga atc ccg atc ggg tgc gtc gcc gga 547 Leu Met Val Asp Gly His Gly Ile Pro Ile Gly Cys Val Val Ala Gly 140 gcc aat cgg cat gat tta ccg ttg tta gct gca acc ttg gac acg ctc 595 Ala Asn Arg His Asp Leu Pro Leu Leu Ala Ala Thr Leu Asp Thr Leu 160 ggc cgg ttt ggg ggc tct ctt ccc gat cag atc acg gtg cat ctc gat 643 Gly Arg Phe Gly Gly Ser Leu Pro Asp Gln Ile Thr Val His Leu Asp 170 175 gct ggg tat gac tcg aag aaa acc cgc agg cta ctc agc gaa ttt ggt 691 Ala Gly Tyr Asp Ser Lys Lys Thr Arg Arg Leu Leu Ser Glu Phe Gly 185 190 tat agc tgg gtg atc agc att aaa ggt gag ccg ctg cag gct ggg act 739 Tyr Ser Trp Val Ile Ser Ile Lys Gly Glu Pro Leu Gln Ala Gly Thr 210 cgg tgg gtg gtg cgt act aac tct tgg cat aac cgg ggt ttt aag 787 Arg Trp Val Val Glu Arg Thr Asn Ser Trp His Asn Arg Gly Phe Lys 215 220 225 aaa ctt agt atc tgc acc gaa cgt tgt acc cgg gtt gtg gaa gcg ttt 835 Lys Leu Ser Ile Cys Thr Glu Arg Cys Thr Arg Val Val Glu Ala Phe 240 atc gct tta gcc aac gcg gtg att att ctg cgt cgg ctt atc aaa cag 883 Ile Ala Leu Ala Asn Ala Val Ile Ile Leu Arg Arg Leu Ile Lys Gln 250 255 gcc tgg act agt tac cgc tgg gac acc cga ccg ggc cac aga cct 928 Ala Trp Thr Ser Tyr Arg Trp Asp Thr Arg Pro Gly His Arg Pro taatctatcc gcgcaatctc taa 951 <210> 258 <211> 276 <212> PRT <213> Corynebacterium glutamicum <400> 258 Val Pro Ala Leu Pro Ser Ser Ile Ile Asp Pro Leu Trp Arg Gln Phe Ser Ala Leu Ile Pro Pro Val Ile Ile Thr His Pro Leu Gly Cys His 25 Arg Ala Arg Ile Ala Asp Arg Ile Ile Val Asp Lys Leu Ile Ala Val

Leu Val Leu Gly Val Ser Tyr Ile Lys Ile Ser Asp Ser Thr Cys Ser

50 60 Ala Thr Thr Ile Arg Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile Phe Lys Asn Leu Glu Gln Ile Cys Leu Glu Ser Tyr Asp Arg Phe Ile 85 90 Gly Leu Asp Leu Glu Asn Leu Asn Val Asp Gly Cys Ile Val Lys Ala 105 Pro Cys Gly Gly Glu Val Ala Gly Arg Phe Pro Val Asp Arg Glu Lys 115 120 Gly Thr Lys Arg Ser Leu Met Val Asp Gly His Gly Ile Pro Ile Gly 135 Cys Val Val Ala Gly Ala Asn Arg His Asp Leu Pro Leu Leu Ala Ala 145 150 Thr Leu Asp Thr Leu Gly Arg Phe Gly Gly Ser Leu Pro Asp Gln Ile Thr Val His Leu Asp Ala Gly Tyr Asp Ser Lys Lys Thr Arg Arg Leu 180 Leu Ser Glu Phe Gly Tyr Ser Trp Val Ile Ser Ile Lys Gly Glu Pro Leu Gln Ala Gly Thr Arg Trp Val Val Glu Arg Thr Asn Ser Trp His 210 215 Asn Arg Gly Phe Lys Lys Leu Ser Ile Cys Thr Glu Arg Cys Thr Arg 230 Val Val Glu Ala Phe Ile Ala Leu Ala Asn Ala Val Ile Ile Leu Arg 245 Arg Leu Ile Lys Gln Ala Trp Thr Ser Tyr Arg Trp Asp Thr Arg Pro 260 265 Gly His Arg Pro 275 <210> 259 <211> 742 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(742) <223> RXN03121 ctaggggtgg cgggattgca aaaatccgtc cccggttcgc catgaaatgc tgattttgat 60

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ccc Pro	: gaa Glu	ggg	tgc Cys	gaa Glu 10	Val	ggc	att Ile	cgt Arg	aga Arg 15	Thr	atc Ile	cca Pro	gag Glu	gaa Glu 20	agc Ser	163
cgt Arg	acg Thr	gct Ala	ttc Phe 25	Leu	gac Asp	atg Met	atc Ile	aat Asn 30	caa Gln	ggt Gly	atg Met	tca Ser	ggt Gly 35	Leu	gct Ala	211
gcg Ala	tct Ser	aca Thr 40	gcg Ala	gtc Val	GJÀ aaa	gtc Val	agt Ser 45	gaa Glu	ttc Phe	acc Thr	Gly	cga Arg 50	aag Lys	tgg Trp	gcg Ala	259
aag Lys	gcc Ala 55	gcc Ala	Gly	gtg Val	aaa Lys	ctg Leu 60	acc Thr	cgc Arg	ggc	ccg Pro	cga Arg 65	ggt Gly	ggc Gly	aat Asn	gct Ala	307
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gga Gly	tgc Cys	cta Leu	ccc Pro	cga Arg 90	gaa Glu	atc Ile	ggc Gly	gag Glu	tat Tyr 95	gtc Val	ggc Gly	atg Met	act Thr	cgg Arg 100	gcc Ala	403
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gca Ala	gcc Ala	acc Thr 120	ttg Leu	cgc Arg	acc Thr	ggc Gly	aag Lys 125	cga Arg	gca Ala	gct Ala	gaa Glu	ttc Phe 130	atc Ile	cac His	gcc Ala	499
Pro	gtg Val 135	atg Met	ggc Gly	cct Pro	tat Tyr	tat Tyr 140	ggg Gly	cca Pro	cgc Arg	aca Thr	ctc Leu 145	cat His	caa Gln	gtg Val	ttg Leu	547
cgt Arg 150	gag Glu	gac Asp	tac Tyr	aca Thr	aca Thr 155	ctg Leu	ttt Phe	gac Asp	gag Glu	tta Leu 160	tct Ser	gcg Ala	ttg Leu	ggg Gly	ttg Leu 165	595
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tta Leu	cgc Arg	Phe	tct Ser 185	tat Tyr	atg Met	tcg Ser	tgt Cys	gta Val 190	gtg Val	ccg Pro	tta Leu	ttt Phe	gct Ala 195	gat Asp	gaa Glu	691
atc Ile	гàг	atc Ile 200	gta Val	gga Gly	caa Gln	Gly	aca Thr 205	cga Arg	tta Leu	tcg Ser	tta Leu	gaa Glu 210	gag Glu	aaa Lys	atg Met	739
atg Met																742

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<213> Corynebacterium glutamicum

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Met Ser Gly Leu Ala Ala Ser Thr Ala Val Gly Val Ser Glu Phe Thr 35 40 45

Gly Arg Lys Trp Ala Lys Ala Ala Gly Val Lys Leu Thr Arg Gly Pro 50 55 60

Arg Gly Gly Asn Ala Phe Asp Thr Ala Glu Lys Leu Glu Ile Ala Ala 65 70 75 80

Ser Met Leu Glu Lys Gly Cys Leu Pro Arg Glu Ile Gly Glu Tyr Val 85 90 95

Gly Met Thr Arg Ala Asn Ile Ser Leu Trp Arg Lys Gln Gly Pro Asp 100 105 110

Lys Leu Arg Gln Arg Ala Ala Thr Leu Arg Thr Gly Lys Arg Ala Ala 115 120 125

Glu Phe Ile His Ala Pro Val Met Gly Pro Tyr Tyr Gly Pro Arg Thr 130 135 140

Leu His Gln Val Leu Arg Glu Asp Tyr Thr Thr Leu Phe Asp Glu Leu 145 150 155 160

Ser Ala Leu Gly Leu Pro Ala Gln Val Cys Gly Ala Leu Leu His Leu 165 170 175

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1 ggt cgg cag ttc cct cgt gaa atc atc ctg tgg gcg gtg cgg tgg tac Gly Arg Gln Phe Pro Arg Glu Ile Ile Leu Trp Ala Val Arg Trp Tyr tgc cgc tac ggc gtg agc tat cgc gac ctc gaa gag atg acc gag 211 Cys Arg Tyr Gly Val Ser Tyr Arg Asp Leu Glu Glu Met Met Thr Glu 259 cgg gga gtg ccg gtc gat cac acc acg atc tac cgc tgg gtc cag aaa Arg Gly Val Pro Val Asp His Thr Thr Ile Tyr Arg Trp Val Gln Lys 307 tat gct cct gag ctg gat aag aag acc cgg tgg tat cgg caa gtt cct Tyr Ala Pro Glu Leu Asp Lys Lys Thr Arg Trp Tyr Arg Gln Val Pro 55 gac tgg cag gcc agg tcc tgg cgg gtg gat gag acc tat atc cgg gtc 355 Asp Trp Gln Ala Arg Ser Trp Arg Val Asp Glu Thr Tyr Ile Arg Val 70 ggg gga aag tgg tgc tac ctc tat cgg gca atc acc gcc ggt agc cag 403 Gly Gly Lys Trp Cys Tyr Leu Tyr Arg Ala Ile Thr Ala Gly Ser Gln acc ctg gac ttc tac ctc tcc ccg aag aga aac gtc gcg gcg gcg aag 451 Thr Leu Asp Phe Tyr Leu Ser Pro Lys Arg Asn Val Ala Ala Ala Lys cgt ttc ctg gcg aag acg ctg cgg tcg aat aat 484 Arg Phe Leu Ala Lys Thr Leu Arg Ser Asn Asn 120 <210> 262 <211> 128 <212> PRT <213> Corynebacterium glutamicum <400> 262 Met Gly Ile Phe Ser Gly Arg Gln Phe Pro Arg Glu Ile Ile Leu Trp Ala Val Arg Trp Tyr Cys Arg Tyr Gly Val Ser Tyr Arg Asp Leu Glu Glu Met Met Thr Glu Arg Gly Val Pro Val Asp His Thr Thr Ile Tyr Arg Trp Val Gln Lys Tyr Ala Pro Glu Leu Asp Lys Lys Thr Arg Trp Tyr Arg Gln Val Pro Asp Trp Gln Ala Arg Ser Trp Arg Val Asp Glu Thr Tyr Ile Arg Val Gly Gly Lys Trp Cys Tyr Leu Tyr Arg Ala Ile Thr Ala Gly Ser Gln Thr Leu Asp Phe Tyr Leu Ser Pro Lys Arg Asn 100 105 110

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ccg Pro	cgg Arg 85	aaa Lys	atg Met	cat His	ggt Gly	ttt Phe 90	aaa Lys	agc Ser	gcg Ala	acg Thr	cag Gln 95	gta Val	tat Tyr	gaa Glu	ata Ile	346
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423

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Ala	Ala	Leu	Ile 20	Pro	Pro	Val	Thr	Asp 25	Thr	His	Pro	Leu	Arg 30	Cys	His	
Arg	Pro	Arg 35	Ile	Pro	Asp	Arg	Ile 40	Ile	Phe	Asp	Lys	Leu 45	Ile	Gln	Val	
Leu	Val 50	Leu	Gly	Ala	Ser	Tyr 55	Ala	Lys	Ile	Ala	Asp 60	Thr	Thr	Cys	Ser	
Ala 65	Thr	Thr	Leu	Arg	Thr 70	Arg	Arg	Asp	Glu	Trp 75	Ile	Thr	Ala	Gly	Ile 80	
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Gly	Leu	Asp	Leu 100													
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cgg Arg	aag Lys	ttc Phe	aag Lys 20	cgc Arg	acg Thr	acc Thr	ggc Gly	agc Ser 25	gat Asp	cat His	acc Thr	ttc Phe	aac Asn 30	atc Ile	gca Ala	96
ccg Pro	aac Asn	ttt Phe 35	ctg Leu	cag Gln	cag Gln	gac Asp	ttt Phe 40	atg Met	gcg Ala	agc Ser	agg Arg	ccg Pro 45	aac Asn	cag Gln	aag Lys	144
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Asn Ile Ile Ala Asp Thr Ile Cys Arg Thr Ala Glu Leu Gly Leu Thr 10 15 20

atc acc ggc gct tcc gat gca ggt gat tac acc ctg atc gaa gca gac 211 Ile Thr Gly Ala Ser Asp Ala Gly Asp Tyr Thr Leu Ile Glu Ala Asp 25 30 35

gca ctc gac tac acc tcc acc tgc cca gaa tgc tcc caa cct ggg gtg 259
Ala Leu Asp Tyr Thr Ser Thr Cys Pro Glu Cys Ser Gln Pro Gly Val
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Phe Arg His His Thr His Arg Met Leu Ile Asp Leu Pro Ile Val Gly
55 60 65

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Phe Pro Thr Lys Leu Phe Ile Arg Leu Pro Arg Tyr Arg Cys Thr Asn
70 80 85

ccc aca tgt aag caa aag tat ttc caa gca gaa cta agc tgc gct gac 403
Pro Thr Cys Lys Gln Lys Tyr Phe Gln Ala Glu Leu Ser Cys Ala Asp
90 95 100

cac ggt aaa aag gtc acc cac cgg gtc acc cgc tgg att tta caa cgc  $\,$  451 His Gly Lys Lys Val Thr His Arg Val Thr Arg Trp Ile Leu Gln Arg  $\,$  105  $\,$  110  $\,$  115

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cta ggg tgg gat tta acc tgc caa cta gcc ctc gat atg tgc cgt gag 547 Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala Leu Asp Met Cys Arg Glu

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					cct Pro 155											595
					tgg Trp											643
					gtc Val											691
					tta Leu											739
					ggc Gly							_		_		787
					gat Asp 235											835
					gct Ala											883
				-	aag Lys			_	_			_		_		931
					cgt Arg											979
					acc Thr											1027
					ttg Leu 315											1075
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					gcg Ala											1171
					ggg Gly											1219
agt Ser	ttg Leu 375	ttt Phe	aaa Lys	cga Arg	ctt Leu	ggt Gly 380	gat Asp	gtg Val	ttg Leu	gcg Ala	tat Tyr 385	ttc Phe	gat Asp	gtt Val	ggt Gly	1267

1315

1363

1408

1431

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cgt Arg	l GJ?	g att / Ile	gct Ala	cta Leu 410	Gly	ttc Phe	cgt Arg	aat Asn	ttg Leu 415	ı Asn	cac His	tac Tyr	att Ile	ctg Leu 420	cgg Arg
tgc Cys	ctt Leu	ato Ile	cat His 425	tca Ser	Gly	cag Gln	ttg Leu	gtc Val 430	His	aag Lys	atc Ile	aat Asn	gca Ala 435	Leu	
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Leu	Ile	Glu 35	Ala	Asp	Ala	Leu	Asp 40	Tyr	Thr	Ser	Thr	Cys 45	Pro	Glu	Cys
Ser	Gln 50	Pro	Gly	Val	Phe	Arg 55	His	His	Thr	His	Arg 60	Met	Leu	Ile	Asp
Leu 65	Pro	Ile	Val	Gly	Phe 70	Pro	Thr	Lys	Leu	Phe 75	Ile	Arg	Leu	Pro	Arg 80
Tyr	Arg	Cys	Thr	Asn 85	Pro	Thr	Cys	Lys	Gln 90	Lys	Tyr	Phe	Gln	Ala 95	Glu
Leu	Ser	Cys	Ala 100	Asp	His	Gly	Lys	Lys 105	Val	Thr	His	Arg	Val 110	Thr	Arg
Trp	Ile	Leu 115	Gln	Arg	Leu	Ala	Ile 120	Asp	Arg	Met	Ser	Val 125	His	Ala	Thr
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Asp 145	Met	Cys	Arg	Glu	Leu 150	Val	Tyr	Asn	Asp	Pro 155	His	His	Leu	Asp	Gly 160
Val	Tyr	Val	Ile	Gly 165	Val	Asp	Glu	His	Lys 170	Trp	Ser	His	Asn	Arg 175	Ala
Lys	His	Gly	Asp 180	Gly	Phe	Val	Thr	Val 185	Ile	Val	Asp		Thr 190	Gly	His
Arg	Tyr	Asp 195	Ser	Arg	Cys	Pro	Ala 200	Arg	Leu	Leu	Asp	Val 205	Val	Pro	Gly

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1 5 atc agg gag cgt ttt acc aat cac ttc gtc aat gcc ggt cac cag gcg 163 Ile Arg Glu Arg Phe Thr Asn His Phe Val Asn Ala Gly His Gln Ala gta cct agc gcg tca ctg att ctc gac gac cct aac ctg ctg ttc gtt 211 Val Pro Ser Ala Ser Leu Ile Leu Asp Asp Pro Asn Leu Leu Phe Val 30 aac gca ggc atg gtt cca ttc aag ccg tac ttc ctg ggc cag cag acc 259 Asn Ala Gly Met Val Pro Phe Lys Pro Tyr Phe Leu Gly Gln Gln Thr 40 cca cct ttt gaa aac ggc act gcg act tcc att cag aag tgt gtt cgt 307 Pro Pro Phe Glu Asn Gly Thr Ala Thr Ser Ile Gln Lys Cys Val Arg 55 acc ctg gat atc gaa gaa gtg ggt atc acc act cgc cac aat acc ttc 355 Thr Leu Asp Ile Glu Glu Val Gly Ile Thr Thr Arg His Asn Thr Phe 70 ttc cag atg gca ggt aac ttc tcc ttc ggc cag tac ttc aaa gaa ggc 403 Phe Gln Met Ala Gly Asn Phe Ser Phe Gly Gln Tyr Phe Lys Glu Gly 90 gca att acc cac gca tgg ggc ctt ctg act ggt tcc gta gca gac gga 451 Ala Ile Thr His Ala Trp Gly Leu Leu Thr Gly Ser Val Ala Asp Gly 105 ggc ttt ggc ctt gat cca gag cgc ctc tgg gtc act gtg tac ctc gat 499 Gly Phe Gly Leu Asp Pro Glu Arg Leu Trp Val Thr Val Tyr Leu Asp 120 gat gac gag gct gca gag atc tgg gaa aag aag atc ggc gtc cca tca 547 Asp Asp Glu Ala Ala Glu Ile Trp Glu Lys Lys Ile Gly Val Pro Ser 135 gag cgc atc cag cgc ctg ggt atg gct gac aac tac tgg tcc atg ggt 595 Glu Arg Ile Gln Arg Leu Gly Met Ala Asp Asn Tyr Trp Ser Met Gly 150 gta cca gga cct tgt ggc cct tgc tcc gag atc tac tac gac cgc ggc 643 Val Pro Gly Pro Cys Gly Pro Cys Ser Glu Ile Tyr Tyr Asp Arg Gly gag aag tac ggc aag gaa ggc ggc cct gtc gct gac gac aac cgc tac 691 Glu Lys Tyr Gly Lys Glu Gly Gly Pro Val Ala Asp Asp Asn Arg Tyr 190 atg gag atc tgg aac ctg gtc ttc atg gag aag gaa cgc gga cag ggt 739 Met Glu Ile Trp Asn Leu Val Phe Met Glu Lys Glu Arg Gly Gln Gly 205 att ggc aag gac aac ttc gac atc ctt ggc gat ctt cca aag aag aac 787 Ile Gly Lys Asp Asn Phe Asp Ile Leu Gly Asp Leu Pro Lys Lys Asn 220 atc gat acc ggc atg ggc gtc gag cgc gtt gcc tgc atc ctc cag gat Ile Asp Thr Gly Met Gly Val Glu Arg Val Ala Cys Ile Leu Gln Asp 230

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Gln Lys Cys Val Arg Thr Leu Asp Ile Glu Glu Val Gly Ile Thr Thr 70 Arg His Asn Thr Phe Phe Gln Met Ala Gly Asn Phe Ser Phe Gly Gln 85 Tyr Phe Lys Glu Gly Ala Ile Thr His Ala Trp Gly Leu Leu Thr Gly Ser Val Ala Asp Gly Gly Phe Gly Leu Asp Pro Glu Arg Leu Trp Val Thr Val Tyr Leu Asp Asp Glu Ala Ala Glu Ile Trp Glu Lys Lys 135 Ile Gly Val Pro Ser Glu Arg Ile Gln Arg Leu Gly Met Ala Asp Asn 155 Tyr Trp Ser Met Gly Val Pro Gly Pro Cys Gly Pro Cys Ser Glu Ile Tyr Tyr Asp Arg Gly Glu Lys Tyr Gly Lys Glu Gly Gly Pro Val Ala 185 Asp Asp Asn Arg Tyr Met Glu Ile Trp Asn Leu Val Phe Met Glu Lys 200 205 Glu Arg Gly Gln Gly Ile Gly Lys Asp Asn Phe Asp Ile Leu Gly Asp 215 Leu Pro Lys Lys Asn Ile Asp Thr Gly Met Gly Val Glu Arg Val Ala 230 235 Cys Ile Leu Gln Asp Val Glu Asn Val Tyr Glu Thr Asp Leu Leu Arg 250 Pro Val Ile Asp Val Ala Glu Thr Leu Thr Gly Thr Lys Tyr Gly Ser 260 265 Asp Asn Thr Ser Asp Ile Arg Phe Arg Val Ile Ala Asp His Ser Arg 280 Thr Gly Met Met Leu Ile Leu Asp Gly Val Thr Pro Gly Asn Glu Gly 290 295 Arg Gly Tyr Ile Leu Arg Arg Leu Leu Arg Arg Ile Ile Arg Ser Ala 310 Arg Leu Leu Gly Ala Thr Gly Glu Thr Met Glu Gln Phe Met Asn Thr 325 Ile Met Asp Thr Met Thr Pro Ser Tyr Pro Glu Ile Ala Asp Asn Arg 340 Glu Arg Ile Met Arg Val Ala Val Thr Glu Glu Arg Ala Phe Leu Lys Thr Leu Val Ser Gly Thr His Leu Phe Glu Glu Ala Ala Thr Ser Ile 370 375

Lys Ala Ala Gly Ser Thr Lys Val Ala Gly Ala Gln Ala Phe Ala Leu 390 His Asp Thr Tyr Gly Phe Pro Ile Asp Leu Thr Leu Glu Met Ala Ala Glu Ala Gly Leu Glu Val Asp Val Glu Gly Phe Asp Ser Leu Met Ala 425 Glu Gln Arg Ser Arg Ala Lys Ala Asp Ser Gln Ala Lys Lys His Gly His Thr Asp Leu Ser Ile Tyr Arg Glu Trp Val Asp Asn Asn Pro Thr 455 Val Phe Thr Gly Phe Glu Glu Leu Asp Ser Gln Ser Lys Val Leu Gly Leu Leu Ser Asp Gly Ala Lys Ile Ser Glu Ala Thr Glu Gly Gln Glu 485 490 Val Glu Val Ile Leu Asp Gln Ser Pro Leu Tyr Ala Glu Ser Gly Gly 505 Gln Leu Gly Asp Arg Gly Gln Ile Leu Leu Gly Asp Thr Val Leu Asp 520 Val His Asp Val Gln Lys Ile Gly Lys Lys Leu Trp Val His Lys Ala 535 Leu Val Ala Asn Gly Gly Leu Ala Val Gly Asp Glu Val Val Ala Ser 550 555 Val Asp Lys Gln Trp Arg His Ala Ala Arg Gln Ala His Thr Ala Thr 565 His Leu Ile His Ala Ala Leu Arg Gln Val Leu Gly Pro Thr Ala Leu 585 Gln Ala Gly Ser Met Asn Lys Pro Gly Tyr Leu Arg Phe Asp Phe Asn 595 Tyr Thr Glu Gln Leu Thr Pro Ala Gln Val Glu Gln Ile Gln Ala Ile Thr Asn Glu Ala Val Asp Thr Asp Trp Ala Val Asn Thr Val Glu Thr Ser Leu Glu Glu Ala Lys Ala Met Gly Ala Met Ala Leu Phe Gly Glu Asn Tyr Gly Ser Thr Val Arg Val Val Glu Ile Gly Gly Pro Phe Ser Met Glu Leu Cys Gly Gly Thr His Val Ala His Ser Ser Gln Ile Gly Pro Val Ala Leu Leu Gly Glu Ser Ser Ile Gly Ser Gly Val Arg Arg 695 Ile Glu Ala Tyr Ser Gly Leu Asn Ser Phe Asn Tyr Leu Ser Lys Glu

705 710 715 720 Arg Ala Leu Ala Glu Gly Leu Ala Ser Ser Leu Lys Ala Pro Ser Glu 730 Glu Leu Pro Glu Arg Val Ala Gln Leu Val Asp Lys Leu Lys Ala Ala 745 Glu Lys Glu Ile Glu Ala Leu His Arg Gln Gln Leu Met Ala Gln Thr Ala Asp Leu Leu Asn Asn Ala Gln Glu Ile Gly Gly Val Thr Thr Leu Leu Leu Arg Val Lys Asp Asn Thr Asn Ala Gly Asp Leu Arg Thr Ile Ala Thr Thr Leu Lys Asp Lys Leu Gly Asp Arg Glu Gly Val Leu Val Ile Ala Ser Asp Asn Ala Gly Lys Val Pro Phe Val Val Ala Ala Thr 825 Lys Ala Ala Val Ala Arg Gly Ala His Ser Gly Asn Leu Val Lys Leu Val Gly Ser Tyr Ile Asp Gly Arg Gly Gly Gly Lys Ala Asp Leu Ala 855 Gln Gly Ser Gly Ala Asn Ile Ala Gly Leu Glu Ser Ala Phe Gly Ala Val Arg Ala Glu Ile Glu Ala Leu 885 <210> 275 <211> 1773 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1750) <223> RXN00975 <400> 275 tatacagaga ccaatgattt ttcattaaaa aggcagggat ttgttataag tatgggtcgt 60 attetgtgcg acgggtgtac etcggetaga atttetecce atg aca eca get gat 115 Met Thr Pro Ala Asp ctc gca aca ttg att aaa gag acc gcg gta gag gtt ttg acc tcc cgc 163 Leu Ala Thr Leu Ile Lys Glu Thr Ala Val Glu Val Leu Thr Ser Arg gag etc gat act tet gtt ett eeg gag eag gta gtt gtg gag egt eeg 211 Glu Leu Asp Thr Ser Val Leu Pro Glu Gln Val Val Glu Arg Pro 25 30

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Ile Ala Leu Gln Val Ala Lys Lys Val Gly Gln Asn Pro Arg Asp Leu 50 55 60

Ala Thr Trp Leu Ala Glu Ala Leu Ala Ala Asp Asp Ala Ile Asp Ser 65 70 75 80

Ala Glu Ile Ala Gly Pro Gly Phe Leu Asn Ile Arg Leu Ala Ala Ala 85 90 95

Ala Gl<br/>n Gly Glu Ile Val Ala Lys Ile Leu Ala Gl<br/>n Gly Glu Thr Phe 100  $\phantom{000}$  105  $\phantom{000}$  110

Gly Asn Ser Asp His Leu Ser His Leu Asp Val Asn Leu Glu Phe Val

Ser Ala Asn Pro Thr Gly Pro Ile His Leu Gly Gly Thr Arg Trp Ala 130 135 140

Ala Val Gly Asp Ser Leu Gly Arg Val Leu Glu Ala Ser Ser Ala Lys 145 150 155 160

Val Thr Arg Glu Tyr Tyr Phe Asn Asp His Gly Arg Gln Ile Asp Arg 165 170 175

Phe Ala Leu Ser Leu Leu Ala Ala Lys Gly Glu Pro Thr Pro Glu 180 185 190

Asp Gly Tyr Gly Gly Glu Tyr Ile Lys Glu Ile Ala Glu Ala Ile Val 195 200 205

Glu Lys His Pro Glu Ala Leu Ala Leu Glu Pro Ala Ala Thr Gln Glu 210 215 220

Leu Phe Arg Ala Glu Gly Val Glu Met Met Phe Glu His Ile Lys Ser 235 230 235

Ser Leu His Glu Phe Gly Thr Asp Phe Asp Val Tyr Tyr His Glu Asn 245 250 Ser Leu Phe Glu Ser Gly Ala Val Asp Lys Ala Val Gln Val Leu Lys Asp Asn Gly Asn Leu Tyr Glu Asn Glu Gly Ala Trp Trp Leu Arg Ser Thr Glu Phe Gly Asp Asp Lys Asp Arg Val Val Ile Lys Ser Asp Gly 295 Asp Ala Ala Tyr Ile Ala Gly Asp Ile Ala Tyr Val Ala Asp Lys Phe Ser Arg Gly His Asn Leu Asn Ile Tyr Met Leu Gly Ala Asp His His 325 330 Gly Tyr Ile Ala Arg Leu Lys Ala Ala Ala Ala Leu Gly Tyr Lys 345 Pro Glu Gly Val Glu Val Leu Ile Gly Gln Met Val Asn Leu Leu Arg 360 Asp Gly Lys Ala Val Arg Met Ser Lys Arg Ala Gly Thr Val Val Thr 375 Leu Asp Asp Leu Val Glu Ala Ile Gly Ile Asp Ala Ala Arg Tyr Ser 395 Leu Ile Arg Ser Ser Val Asp Ser Ser Leu Asp Ile Asp Leu Gly Leu 410 Trp Glu Ser Gln Ser Ser Asp Asn Pro Val Tyr Tyr Val Gln Tyr Gly 425 His Ala Arg Leu Cys Ser Ile Ala Arg Lys Ala Glu Thr Leu Gly Val 435 445 Thr Glu Glu Gly Ala Asp Leu Ser Leu Leu Thr His Asp Arg Glu Gly Asp Leu Ile Arg Thr Leu Gly Glu Phe Pro Ala Val Val Lys Ala Ala 475 Ala Asp Leu Arg Glu Pro His Arg Ile Ala Arg Tyr Ala Glu Glu Leu Ala Gly Thr Phe His Arg Phe Tyr Asp Ser Cys His Ile Leu Pro Lys 500 505 Val Asp Glu Asp Thr Ala Pro Ile His Thr Ala Arg Leu Ala Leu Ala Ala Ala Thr Arg Gln Thr Leu Ala Asn Ala Leu His Leu Val Gly Val 530 540 Ser Ala Pro Glu Lys Met 545

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Asp Ser Ser Leu Asp Ile Asp Leu Gly Leu Trp Glu Ser Gln Ser Ser 195 200 205

Asp Asn Pro Val Tyr Tyr Val Gln Tyr Gly His Ala Arg Leu Cys Ser 210 215 220

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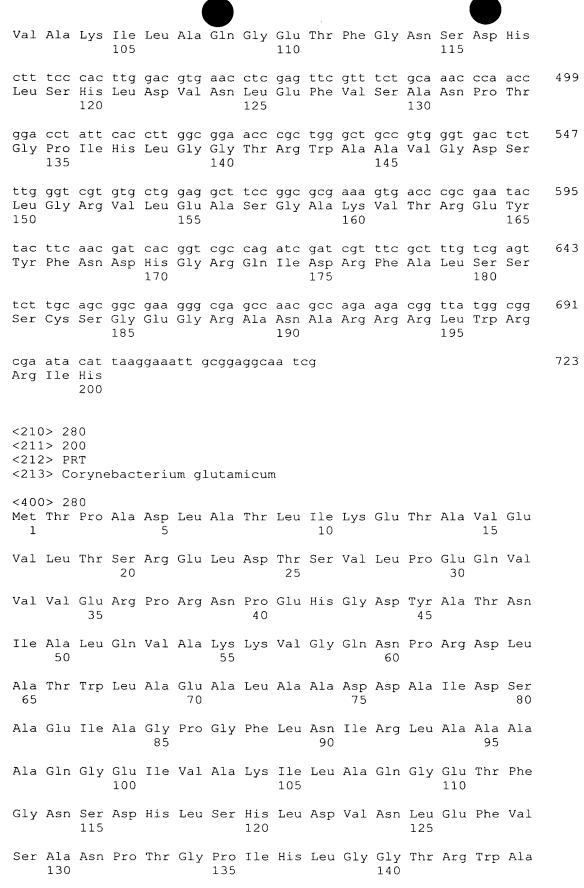
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gtg gcc aag att ctg gca cag ggc gag act ttc gga aac tcc gat cac 451



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aag Lys 150	ATO	gca Ala	a cgo a Aro	e acc	gto Val	Leu	gac Asp	ago Ser	cac His	gat Asp 160	) Phe	acc Thr	gaç Glu	g ato	gag Glu 165	595
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330

310

325

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Val Leu Arg Thr His

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Glu Glu Ala Arg Glu Lys Phe Gly Phe Leu Leu Asp Ala Phe Ala Phe 520 Gly Ala Pro Pro His Gly Gly Ile Ala Phe Gly Trp Asp Arg Ile Val 535 Ser Leu Leu Gly Gly Phe Asp Ser Ile Arg Asp Val Ile Ala Phe 550 <210> 285 <211> 1503 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1480) <223> RXA00314 <400> 285 agcgggagcc aacctgctca acgtcgcaaa gaaagaagcg gtgccagcaa caccataagt 60 tgaaaccttg agtgttcgca cacaggttag actaggggac gtg act cta cgc atc Val Thr Leu Arg Ile 1 ttt gac acc ggt acc cgt acg ctt cga gat ttt aaa cct gtt caa cca Phe Asp Thr Gly Thr Arg Thr Leu Arg Asp Phe Lys Pro Val Gln Pro 10 ggt cat gcc tcg gtg tac ctg tgt ggt gcc acc ccg caa tct tca ccc 211 Gly His Ala Ser Val Tyr Leu Cys Gly Ala Thr Pro Gln Ser Ser Pro 25 cac att gga cat gtt cgt tca gca gta gcg ttt gat att ttg cgc cgc 259 His Ile Gly His Val Arg Ser Ala Val Ala Phe Asp Ile Leu Arg Arg 40 tgg ctc atg gct aag gga ctt gat gtg gca ttt gtt cgc aat gtc act 307 Trp Leu Met Ala Lys Gly Leu Asp Val Ala Phe Val Arg Asn Val Thr 55 60 gat atc gat gac aag att ctc acc aag gca tct gaa aat ggt cgc cct 355 Asp Ile Asp Asp Lys Ile Leu Thr Lys Ala Ser Glu Asn Gly Arg Pro 70 tgg tgg gaa tgg gtg tcc acc tat gaa cgt gaa ttc acc tgg acg tac 403 Trp Trp Glu Trp Val Ser Thr Tyr Glu Arg Glu Phe Thr Trp Thr Tyr 90 aac acg ttg ggt gtg ctt cct cca tca acg gag cct cgt gca aca ggc 451 Asn Thr Leu Gly Val Leu Pro Pro Ser Thr Glu Pro Arg Ala Thr Gly 105 cac gtc act cag atg att aag tac atg cag cgc ttg att gat aac ggc 499 His Val Thr Gln Met Ile Lys Tyr Met Gln Arg Leu Ile Asp Asn Gly 120 125 ttt gct tac gcc gtt gat ggc tct gtg tac ttt gat gtc gca gcg tgg 547

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Gly Lys Arg Gly Pro Gln Asp Phe Ala Leu Trp Lys Ala Ala Lys Pro 185 Gly Glu Pro Ser Trp Pro Thr Pro Trp Gly Asp Gly Arg Pro Gly Trp 200 His Leu Glu Cys Ser Ala Met Ala Thr Tyr Tyr Leu Gly Glu Gln Phe 215 Asp Ile His Cys Gly Gly Leu Asp Leu Gln Phe Pro His His Glu Asn 230 235 Glu Ile Ala Gln Ala His Ala Ala Gly Asp Lys Phe Ala Asn Tyr Trp 245 Met His Asn His Trp Val Thr Met Ala Gly Glu Lys Met Ser Lys Ser 265 Leu Gly Asn Val Leu Ala Val Pro Glu Met Leu Lys Gln Val Arg Pro Val Glu Leu Arg Tyr Tyr Leu Gly Ser Ala His Tyr Arg Ser Val Leu 295 Glu Tyr Ser Glu Ser Ala Leu Ser Glu Ala Ala Val Gly Tyr Arg Arg 310 Ile Glu Ser Phe Leu Glu Arg Val Gly Asp Val Glu Val Gly Glu Trp 325 330 Thr Pro Gly Phe Glu Val Ala Met Asp Glu Asp Ile Ala Val Pro Lys 340 Ala Leu Ala Glu Ile His Asn Ala Val Arg Glu Gly Asn Ala Ala Leu Asp Lys Gly Asp Arg Glu Ala Ala Glu Lys Leu Ala Ser Ser Val Arg 375 Ala Met Thr Gly Val Leu Gly Phe Asp Pro Val Glu Trp Gly Ser Asp 390 395 Ala Gly Ala Asp Gly Lys Ala Asp Lys Ala Leu Asp Val Leu Ile Ser 405 Ser Glu Leu Glu Arg Arg Ala Thr Ala Arg Ala Glu Lys Asn Trp Ala 425 Val Ala Asp Glu Val Arg Asp Arg Leu Ala Asp Ala Gly Ile Glu Val 435

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Gly Ile Thr Pro Tyr Asp Ser Thr His Leu Gly His Ala Ala Thr Tyr 50 55 60

Leu Ala Phe Asp Leu Ile Tyr Arg Ile Leu Leu Asp Asn Asp His Asp 65 70 75 80

Val His Tyr Val Gln Asn Ile Thr Asp Val Asp Asp Pro Leu Phe Glu 85 90 95

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Lys Asp Tyr Ile Gly Ala Ile Glu Ser Ile Asp Glu Val Ile Glu Met 130 135 140

Val Lys Thr Leu Leu Asp Glu Gly Ala Ala Tyr Ile Val Glu Asp Ala 145 150 155 160

Glu Tyr Pro Asp Val Tyr Ala Ser Ile Asn Ala Thr Asp Lys Phe Gly 165 170 175

Tyr Glu Ser Asn Tyr Asp Ala Ala Thr Met Ala Glu Phe Phe Ala Glu 180 185 190

Arg Gly Gly Asp Pro Glu Arg Pro Gly Lys Lys Asn Pro Met Asp Ala 195 200 205

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Phe Gly Ala Gly Arg Pro Gly Trp His Ile Glu Cys Ser Ala Ile Ala 225 230 235 240

Thr Asn Arg Leu Gly His Ser Phe Asp Ile Gln Gly Gly Gly Ser Asp 245 250 255

Leu Ile Phe Pro His His Glu Phe Ser Ala Ala His Ala Glu Ala Ala 260 265 270

His Gly Val Glu Arg Met Ala Lys His Tyr Val His Ala Gly Met Ile
275 280 285

Ser Gln Asp Gly Val Lys Met Ser Lys Ser Leu Gly Asn Leu Glu Phe 290 295 300

Val Ser Arg Leu Thr Ala Ala Gly His Glu Pro Gly Ala Ile Arg Leu

305 310 315 320 Gly Val Phe Ala Asn His Tyr Arg Gly Asn Arg Asp Trp Asn Ala Glu 325 Ser Leu Ala Thr Ala Glu Gln Arg Leu Ala Thr Trp Arg Glu Ala Ala Arg Ala Ala Thr Asn Arg Glu Asp Ala Ile Ala Val Val Glu Gln Leu Arg Ala His Leu Ser Ala Asp Leu Asp Thr Pro Gly Ala Leu Ala Ala 375 Val Asp Asn Trp Ala Ala Gly Ile Asp Thr Thr Thr Asp Ser Lys Glu 395 Phe Thr Glu Val Gly Asn Ile Val Val Ala Ala Ile Asp Ala Leu Leu 405 Gly Val Gln Leu 420 <210> 289 <211> 1532 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(1509) <223> RXA01124 <400> 289 cgg tgg gtg cgg gct att aac atg gcc tgc atg act gat gtt cgt gtt Arg Trp Val Arg Ala Ile Asn Met Ala Cys Met Thr Asp Val Arg Val cgt ttc tgc cca tcg ccc acc ggc acc cca cac gtt gga ctt gtg cgc 96 Arg Phe Cys Pro Ser Pro Thr Gly Thr Pro His Val Gly Leu Val Arg acc gcg ctg ttc aac tgg gca tat gct cgc cac act gga ggc aag tta 144 Thr Ala Leu Phe Asn Trp Ala Tyr Ala Arg His Thr Gly Gly Lys Leu gtt ttc cgc att gag gac act gac gct gcc cgc gat tcc gag gag tct 192 Val Phe Arg Ile Glu Asp Thr Asp Ala Ala Arg Asp Ser Glu Glu Ser 55 tac tee gee ate ate gat tee etg ege tgg ttg gga atg gac tgg gat 240 Tyr Ser Ala Ile Ile Asp Ser Leu Arg Trp Leu Gly Met Asp Trp Asp 70 gag ggt gtg gaa aag ggc ggc ccg cat gag ccc tac cgc cag tcg cag 288 Glu Gly Val Glu Lys Gly Gly Pro His Glu Pro Tyr Arg Gln Ser Gln cgc aag gac atc tat cag gat gtg ttg aag cag ctt atc gac gcc ggt Arg Lys Asp Ile Tyr Gln Asp Val Leu Lys Gln Leu Ile Asp Ala Gly

			100	)				105					110			
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Val Phe Arg Ile Glu Asp Thr Asp Ala Ala Arg Asp Ser Glu Glu Ser 50 55 60

Tyr Ser Ala Ile Ile Asp Ser Leu Arg Trp Leu Gly Met Asp Trp Asp

65 70 75 80 Glu Gly Val Glu Lys Gly Gly Pro His Glu Pro Tyr Arg Gln Ser Gln Arg Lys Asp Ile Tyr Gln Asp Val Leu Lys Gln Leu Ile Asp Ala Gly Glu Val Tyr Pro Ala Tyr Ser Thr Ala Glu Glu Val Glu Glu Arg His Lys Ala Ala Gly Arg Asp Pro Lys Leu Gly Tyr Asp Asn Phe Asp Arg Asp Leu Thr Glu Glu Gln Val Ala Ala Phe Glu Ala Glu Gly Arg Lys 150 155 Pro Val Trp Arg Leu Arg Met Pro Glu Gln Asp Trp Lys Trp Thr Asp 165 170 Leu Val Arg Gly Glu Val Glu Phe Lys Ser Phe Thr Gln Pro Asp Phe 185 Val Val Ala Arg Ser Asn Gly Glu Pro Leu Tyr Thr Leu Val Asn Pro 200 Val Asp Asp Ala Leu Met Glu Val Thr His Val Leu Arg Gly Glu Asp 215 Leu Leu Pro Ser Thr Pro Arg Gln Leu Ala Leu Tyr Glu Ala Leu Lys 230 Arg Ile Gly Val Ala Lys Ala Thr Pro Ala Phe Gly His Leu Pro Phe 245 Val Met Gly Glu Gly Asn Lys Lys Leu Ser Lys Arg Asp Pro Gln Ser 260 265 Ser Leu Phe Asn His Arg Asp Asn Gly Ile Ile Pro Glu Gly Met Leu 280 Asn Tyr Leu Ala Leu Leu Gly Trp Ser Leu Ser Ala Asp Gln Asp Ile 290 295 Phe Gly Val Asp Glu Leu Ile Ala Asn Phe Asp Val Ala Asp Val Leu Gly Asn Pro Ala Arg Phe Asp Gln Lys Lys Leu Glu Ala Ile Asn Ala Asp His Ile Arg Leu Leu Glu Pro Lys Asp Phe Glu Ala Arg Leu Arg Ala Tyr Met Thr Glu Tyr Thr Glu Phe Pro Ala Asp Tyr Pro Ala Glu 360 Lys Phe Ala Ile Ala Ala Glu Leu Val Gln Thr Arg Ile Lys Val Leu Ser Glu Ala Trp Asp Leu Leu Lys Phe Leu Val Thr Ala Asp Glu Asp 390 395 400

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Lys Leu Asp Thr Tyr Glu Cys Tyr Cys Ser Arg Arg Asp Ile Gln Glu gcc tcg cgg gca ccc cat gtg gct ccg gga gtg tat ccg gga acg tgt 451 Ala Ser Arg Ala Pro His Val Ala Pro Gly Val Tyr Pro Gly Thr Cys agg gga ttg aag gag gaa cgc gtc gaa aag cgt gca acc ttg gct 499 Arg Gly Leu Lys Glu Glu Glu Arg Val Glu Lys Arg Ala Thr Leu Ala 125 130 gcg caa aac cgg cac ccc gcc att cgc ctg cgc gcg cag gta acc tcg Ala Gln Asn Arg His Pro Ala Ile Arg Leu Arg Ala Gln Val Thr Ser 140 145 ttt gat ttt cac gac cga ctt cgc ggc cca caa act ggc ccc gta gac 595 Phe Asp Phe His Asp Arg Leu Arg Gly Pro Gln Thr Gly Pro Val Asp 155 160 gat ttc att ctg ctc cgc ggc ggg cag gaa ccc gga tgg gca tac aac Asp Phe Ile Leu Leu Arg Gly Gly Gln Glu Pro Gly Trp Ala Tyr Asn 170 175 180 tta act gtc gtc gtc gac gat gcc tac caa ggc gtt gac cag gta gtc 691 Leu Thr Val Val Val Asp Asp Ala Tyr Gln Gly Val Asp Gln Val Val 185 195 cgc ggc gac gac cta ctc gaa ttc ggc gcg cgc caa gct acc ttg 736 Arg Gly Asp Asp Leu Leu Glu Phe Gly Ala Arg Gln Ala Thr Leu <210> 292 <211> 212 <212> PRT <213> Corynebacterium glutamicum Met Ala Gly Arg Tyr Ala Pro Ser Pro Ser Gly Asp Leu His Phe Gly Asn Leu Arg Thr Ala Leu Leu Ala Trp Leu Phe Ala Arg Ser Glu Gly Lys Lys Phe Leu Met Arg Val Glu Asp Ile Asp Glu Gln Arg Ser Ser Lys Glu Ser Ala Glu Ser Gln Leu Ala Asp Leu Ser Ala Leu Gly Leu Asp Trp Asp Gly Asp Val Leu Tyr Gln Ser Thr Arg Tyr Asp Ala Tyr Arg Ala Ala Leu Glu Lys Leu Asp Thr Tyr Glu Cys Tyr Cys Ser Arg Arg Asp Ile Gln Glu Ala Ser Arg Ala Pro His Val Ala Pro Gly Val Tyr Pro Gly Thr Cys Arg Gly Leu Lys Glu Glu Glu Arg Val Glu Lys 115

Arg Ala Thr Leu Ala Ala Gln Asn Arg His Pro Ala Ile Arg Leu Arg 1.35 Ala Gln Val Thr Ser Phe Asp Phe His Asp Arg Leu Arg Gly Pro Gln Thr Gly Pro Val Asp Asp Phe Ile Leu Leu Arg Gly Gly Gln Glu Pro 165 Gly Trp Ala Tyr Asn Leu Thr Val Val Val Asp Asp Ala Tyr Gln Gly Val Asp Gln Val Val Arg Gly Asp Asp Leu Leu Glu Phe Gly Ala Arg 200 Gln Ala Thr Leu 210 <210> 293 <211> 328 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(328) <223> FRXA00458 <400> 293 cacccctgaa aacctcctca actatcccgg agtgatcatc tccaccgttc aggagaaccc 60 atccgaaaca tggcggcaag tgaacatcta atctagaaac atg gca gga cga tac 115 Met Ala Gly Arg Tyr gca cca tca cca agc ggc gac ctt cac ttt ggc aac ctc cgc aca gca 163 Ala Pro Ser Pro Ser Gly Asp Leu His Phe Gly Asn Leu Arg Thr Ala 15 ctg ctg gcc tgg ctg ttc gcg cgc tcc gaa gga aaa aaa ttc ctc atg 211 Leu Leu Ala Trp Leu Phe Ala Arg Ser Glu Gly Lys Lys Phe Leu Met cgg gtc gaa gac atc gat gaa caa cgc tca ttc aag gaa tcc gcc gaa 259 Arg Val Glu Asp Ile Asp Glu Gln Arg Ser Phe Lys Glu Ser Ala Glu age caa ete gea gae eta tee gee etg ggt ete gat tgg gat gge gae 307 Ser Gln Leu Ala Asp Leu Ser Ala Leu Gly Leu Asp Trp Asp Gly Asp 60 gtc ctc tac caa tcc aca cgc 328 Val Leu Tyr Gln Ser Thr Arg 75

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- ccg ctg ggt gtg gag ctg aag gaa aac atc aag cgc cag tgg tgg cgt 259
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- atc ctt cct cgc cag gtg tgg gta act tcc ggc cac gtt gag gtc ttc

  Ile Leu Pro Arg Gln Val Trp Val Thr Ser Gly His Val Glu Val Phe
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- gac cac ctg ctg gag cag tac gaa gag aag cat ggt cac cca cct gta 451

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Gly Gln Pro Gly Asn Trp Thr Glu Pro Lys Ala Phe Ser Gly Leu Leu 135 Lys Thr Phe Leu Gly Pro Val Asp Asp Glu Glu Gly Leu His Tyr Leu 155 Arg Pro Glu Thr Ala Gln Gly Ile Phe Val Asn Phe Lys Asn Val Met 170 Asn Thr Ser Arg Met Lys Pro Pro Phe Gly Ile Ala Asn Ile Gly Lys 185 Ser Phe Arg Asn Glu Ile Thr Pro Gly Asn Phe Ile Phe Arg Thr Arg Glu Phe Glu Gln Met Glu Met Glu Phe Phe Val Lys Pro Gly Glu Asp 215 Glu Glu Trp His Gln His Trp Ile Asp Thr Arg Leu Gln Trp Tyr Ile 235 Asn Leu Gly Ile Lys Pro Glu Asn Leu Arg Leu Tyr Glu His Pro Gln 250 Glu Lys Leu Ser His Tyr Ser Lys Arg Thr Val Asp Ile Glu Tyr Ala 265 Phe Asn Phe Ala Asn Thr Lys Trp Gly Glu Leu Glu Gly Ile Ala Asn Arg Thr Asp Tyr Asp Leu Arg Val His Ser Glu Gly Ser Gly Glu Asp Leu Ser Phe Phe Asp Gln Glu Thr Asn Glu Arg Trp Ile Pro Phe Val 315 Ile Glu Pro Ala Ala Gly Leu Gly Arg Ala Met Met Phe Leu Met Asp Ala Tyr His Glu Asp Glu Ala Pro Asn Ser Lys Gly Gly Val Asp Lys Arg Val Val Leu Lys Leu Asp Arg Leu Ala Pro Val Lys Val Ala Val Leu Pro Leu Ser Lys Lys Asp Thr Leu Thr Pro Leu Ala Glu 370 Lys Leu Ala Ala Glu Leu Arg Glu Phe Trp Asn Val Asp Tyr Asp Thr Ser Gly Ala Ile Gly Arg Arg Tyr Arg Arg Gln Asp Glu Ile Gly Thr 405 410 Pro Phe Cys Val Thr Val Asp Phe Asp Ser Leu Glu Asp Asn Ala Val Thr Val Arg Glu Arg Asp Thr Met Glu Gln Val Arg Val Pro Leu Asp Glu Leu Gln Gly Tyr Leu Ala Gln Arg Leu Ile Gly Cys

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Ala Val Arg Asp Ala Phe Val Asn Gln Ala His Lys Ala Gly Phe Glu 35 40 45

His Ile Glu Leu Pro Ile Phe Glu Asp Thr Gly Leu Phe Ala Arg Gly 50 55 60

Val Gly Glu Ser Thr Asp Val Val Ser Lys Glu Met Tyr Thr Phe Ala 65 70 75 80

Asp Arg Gly Glu Arg Ser Val Thr Leu Arg Pro Glu Gly Thr Ala Gly 85 90 95

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Val Lys Leu Asn Tyr Ala Gly Pro Phe Phe Arg Tyr Glu Arg Pro Gln
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Ala Gly Arg Tyr Arg Gln Leu Gln Gln Val Gly Val Glu Ala Ile Gly 130 140

Val Asp Asp Pro Ala Leu Asp Ala Glu Ile Ile Ala Leu Ala Asp Arg 145 150 155 160

Ser Tyr Arg Ser Leu Gly Leu Gln Asp Phe Arg Leu Glu Leu Thr Ser 165 170 175

Leu Gly Asp Arg His Cys Arg Pro Glu Tyr Arg Gln Lys Leu Gln Asp 180 185 190

Phe Leu Phe Ala Leu Pro Leu Asp Glu Glu Thr Arg Lys Arg Ala Glu 195 200 205

Ile Asn Pro Leu Arg Val Leu Asp Asp Lys Arg Pro Glu Val Gln Glu 210 215 220

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Arg Glu His Phe Glu Thr Val Thr Gly Leu Leu Asp Asp Met Gly Val 245 250 255

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cc. Pro	a gto Val 299	T TT6	c cca e Pro	a gto o Val	g gad L Asp	ato 11e 300	e Asp	c ggo	c aad / Lys	j tto s Phe	c acc e Thi	c Gly	tto Lei	g gtt ı Val	cct Pro	1027
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gac Asp 630	gtg Val	ctg Leu	gac Asp	cgc Arg	tac Tyr 635	atc Ile	ctg Leu	gcg Ala	aag Lys	ctg Leu 640	cac His	gat Asp	ttg Leu	gtg Val	gca Ala 645	2035
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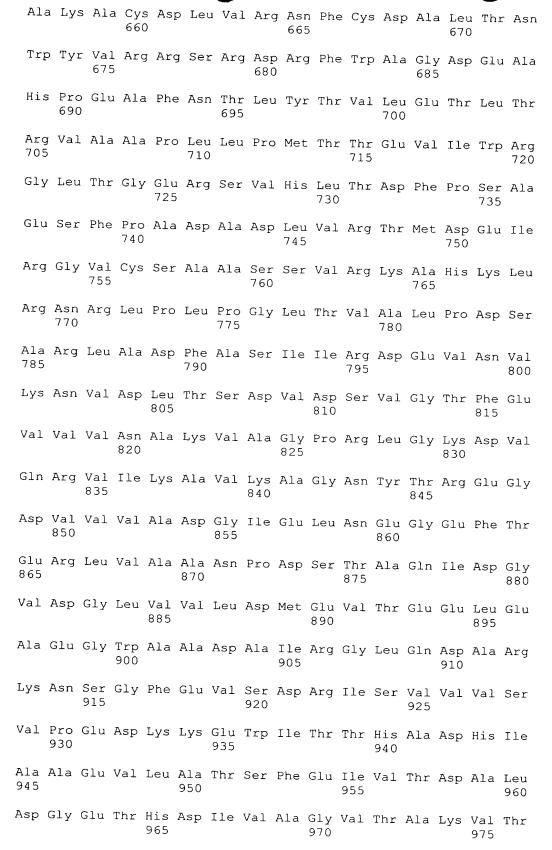
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Gln Thr Ile Glu His Ser Tyr Pro His Ser Trp Arg Ser Gly Glu Pro 345 Leu Ile Tyr Met Ala Leu Pro Ser Trp Phe Val Asn Val Thr Glu Ile 360 Arg Asp Arg Met Val Glu Val Asn Gln Asp Ile Glu Trp Met Pro Ala 375 His Ile Arg Asp Gly Gln Phe Gly Lys Trp Leu Glu Gly Ala Arg Asp 390 Trp Asn Ile Ser Arg Ser Arg Tyr Trp Gly Ser Pro Ile Pro Ala Trp Val Ser Asp Asn Asp Glu Tyr Pro Arg Val Asp Val Tyr Gly Ser Leu Asp Glu Leu Glu Ala Asp Phe Gly Val Arg Pro Lys Ser Leu His Arg Pro Asp Ile Asp Glu Leu Thr Arg Pro Asn Pro Asp Asp Pro Thr Gly Lys Ser Thr Met Arg Arg Val Thr Asp Val Leu Asp Val Trp Phe Asp 470 475 Ser Gly Ser Met Pro Phe Ala Gln Val His Tyr Pro Phe Glu Asn Lys 490 Glu Trp Phe Asp Thr His Ala Pro Ala Asp Phe Ile Val Glu Tyr Ile 500 Gly Gln Thr Arg Gly Trp Phe Tyr Leu Leu His Val Leu Ser Thr Ala Leu Phe Asp Arg Pro Ala Phe Lys Lys Val Val Ala His Gly Ile Val 535 Leu Gly Asp Asp Gly Leu Lys Met Ser Lys Ser Lys Gly Asn Tyr Pro 550 Asn Val Asn Glu Val Phe Asp Arg Asp Gly Ser Asp Ala Met Arg Trp Phe Leu Met Ser Ser Pro Ile Leu Arg Gly Gly Asn Leu Ile Val Thr 585 Glu Lys Gly Ile Arg Glu Gly Val Arg Gln Ala Gln Leu Pro Met Trp Asn Ala Tyr Ser Phe Leu Gln Leu Tyr Thr Ser Lys Asn Ala Thr Trp 615 Ser Val Asp Ser Thr Asp Val Leu Asp Arg Tyr Ile Leu Ala Lys Leu 635 His Asp Leu Val Ala Glu Thr Gln Ala Ala Leu Asp Gly Thr Asp Ile

650

645



Lys Asn

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Ala Asp Gly Lys Ala Leu Pro Glu Asp Lys Leu Phe Val Gln Asp Met 50 55 60

Phe Pro Tyr Pro Ser Gly Ala Gly Leu His Val Gly His Pro Leu Gly 65 70 75 80

Tyr Ile Ala Thr Asp Val Phe Ala Arg Tyr Asn Arg Met Leu Gly Lys  $85 \hspace{1cm} 90 \hspace{1cm} 95$ 

Asn Val Leu His Thr Leu Gly Tyr Asp Ala Phe Gly Leu Pro Ala Glu 100 105 110

Gln Tyr Ala Ile Gln Thr Gly Thr His Pro Arg Thr Thr Met Ala 115 120 125

Asn Ile Glu Asn Met Lys Arg Gln Leu Gly Ala Leu Gly Leu Gly His 130 135 140

Asp Ser Arg Arg Ala Val Ala Thr Thr Asp Pro Glu Phe Tyr Lys Trp 145 150 155 160

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115

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1061

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Ser Lys Glu Pro Tyr Arg Arg Leu Tyr Asn Gln Gly Tyr Ile Gln Ala 65 70 75 80

Phe Ala Tyr Thr Asp Ser Arg Gly Val Tyr Val Pro Ala Asp Asp Val 85 90 95

Glu Glu Lys Asp Gly Lys Phe Phe Tyr Gln Gly Glu Glu Val Asn Gln 100 105 110

Glu Tyr Gly Lys Met Gly Lys Ser Leu Lys Asn Ala Val Ala Pro Asp 115 120 125

Asp Ile Cys Asn Asn Phe Gly Ala Asp Thr Leu Arg Val Tyr Glu Met 130 135 140

Ala Met Gly Pro Leu Asp Thr Ser Arg Pro Trp Ala Thr Lys Asp Val 145 150 155 160

Val Gly Ala Gln Arg Phe Leu Gln Arg Leu Trp Arg Leu Val Val Asp 165 170 175

Glu Asn Thr Gly Glu Val Leu Thr Arg Asp Glu Val Leu Thr Asp Asp 180 185 190

Asp Asn Lys Gln Leu His Arg Thr Ile Ala Gly Val Arg Asp Asp Tyr 195 200 205

Thr Asn Leu Arg Val Asn Thr Val Val Ala Lys Leu Ile Glu Tyr Val 210 215 220

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Trp Lys Lys Leu Gly His Asp Asp Thr Val Thr Tyr Glu Pro Phe Pro 50 60	
Thr Phe Glu Glu Lys Trp Leu Thr Asp Asp Glu Ile Glu Leu Pro Val 65 70 75 80	

115

130

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135

384

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Ala Ser Ile Ala Ala Lys Ser Asp Leu Glu Arg Gln Glu Asn Lys Glu 100 105 110

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Asp Gln Ile Thr Val Phe Ile Ala Asp Tyr Val Leu Thr Gly Tyr Gly 130 135 140

Thr Gly Ala Ile Met Ala Val Pro Ala His Asp Glu Arg Asp Tyr Glu 145 150 155 160

Phe Ala Thr Val Leu Gly Leu Pro Ile Lys Glu Val Val Ala Gly Gly 165 170 175

Asn Ile Glu Glu Ala Ala Phe Thr Glu Ser Gly Glu Ala Val Asn Ser 180 185 190

Ala Asn Asp Asn Gly Leu Asp Ile Asn Gly Leu Ala Lys Asp Glu Ala 195 200 205

Ile Ala Lys Thr Ile Glu Trp Leu Glu Glu Lys Glu Leu Gly Arg Gly 210 215 220

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Trp Gly Glu Pro Phe Pro Ile Val Tyr Asp Glu Asn Gly Gln Ala His  $245 \hspace{1cm} 250 \hspace{1cm} 255$ 

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Tyr Lys Pro Val Ser Phe Asp Pro Glu Asp Ala Asp Ser Glu Pro Ser 275 280 285

Pro Pro Leu Ala Lys Ala Arg Glu Trp Val Glu Val Glu Leu Asp Leu 290 295 300

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Pro Val Glu Val Asp Arg Thr Ile Ser Ile Ser Asp Leu Arg Ser Gln
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70 75

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cac ege tac ace gac etc atc atg ege gaa caa gee ege ace ace geg
His Arg Tyr Thr Asp Leu Ile Met Arg Glu Gln Ala Arg Thr Asn Ala
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Asp Phe Leu Thr Ala Met Glu Gln Gly Met Pro Pro Thr Ser Gly Asn 485 495 Gly Met Gly Ile Asp Arg Leu Leu Met Ala Leu Thr Gly Leu Gly Ile Arg Glu Thr Val Leu Phe Pro Met Val Lys Pro Glu Gln Lys 515 520 525 <210> 315 <211> 619 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(619) <223> RXA02015 <400> 315 eccagagtte gttgagaceg aacaetteet getegaeetg ceageaetgg etgaageaet 60 aaccgagtgg ctgaagggac gcgaagactg gcgtccaaac gtg ttg aag ttc tcg 115 Val Leu Lys Phe Ser 1 ctc aac ctg ctg gac gat atc cgc cca cgc gca atg tcg cgc gat atc 163 Leu Asn Leu Leu Asp Asp Ile Arg Pro Arg Ala Met Ser Arg Asp Ile 10 15 gac tgg ggc atc cca atc cca gtt gaa gga tgg caa gac aac aac gcc 211 Asp Trp Gly Ile Pro Ile Pro Val Glu Gly Trp Gln Asp Asn Asa Ala 25 aag aag ctc tac gtc tgg ttc gac gct gtc gtg ggc tac ttg tcc gca 259 Lys Lys Leu Tyr Val Trp Phe Asp Ala Val Val Gly Tyr Leu Ser Ala 40 50 tee ate gaa tgg gee tae ege tee gge gae eea gaa gea tgg ege ace 307 Ser Ile Glu Trp Ala Tyr Arg Ser Gly Asp Pro Glu Ala Trp Arg Thr 55 ttc tgg aat gat cca gaa acc aag tcc tac tac ttc atg ggc aaa gac 355 Phe Trp Asn Asp Pro Glu Thr Lys Ser Tyr Tyr Phe Met Gly Lys Asp 70 75 80 aac atc acc ttc cac tcc cag atc tgg cca gcg gag ctt ctc ggc tac 403 Asn Ile Thr Phe His Ser Gln Ile Trp Pro Ala Glu Leu Leu Gly Tyr 90 100 gca ggc aag ggc tcc cgc ggt gga gaa atc ggt gac ctg ggt gtt ctg 451 Ala Gly Lys Gly Ser Arg Gly Gly Glu Ile Gly Asp Leu Gly Val Leu 105 110 aac ctg cct act gag gtt gtt tcc tct gag ttc ctg act atg tct gga 499 Asn Leu Pro Thr Glu Val Val Ser Ser Glu Phe Leu Thr Met Ser Gly 120 125 tcc aag ttc tcc tca tcc aag ggc gtt gtc atc tac gtg aag gac ttc 547

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Gly Tyr Leu Ser Ala Ser Ile Glu Trp Ala Tyr Arg Ser Gly Asp Pro 50 55 60

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Phe Met Gly Lys Asp Asn Ile Thr Phe His Ser Gln Ile Trp Pro Ala 85 90 95

Glu Leu Leu Gly Tyr Ala Gly Lys Gly Ser Arg Gly Gly Glu Ile Gly
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Asp Leu Gly Val Leu Asn Leu Pro Thr Glu Val Val Ser Ser Glu Phe 115 120 125

Leu Thr Met Ser Gly Ser Lys Phe Ser Ser Ser Lys Gly Val Val Ile 130 135 140

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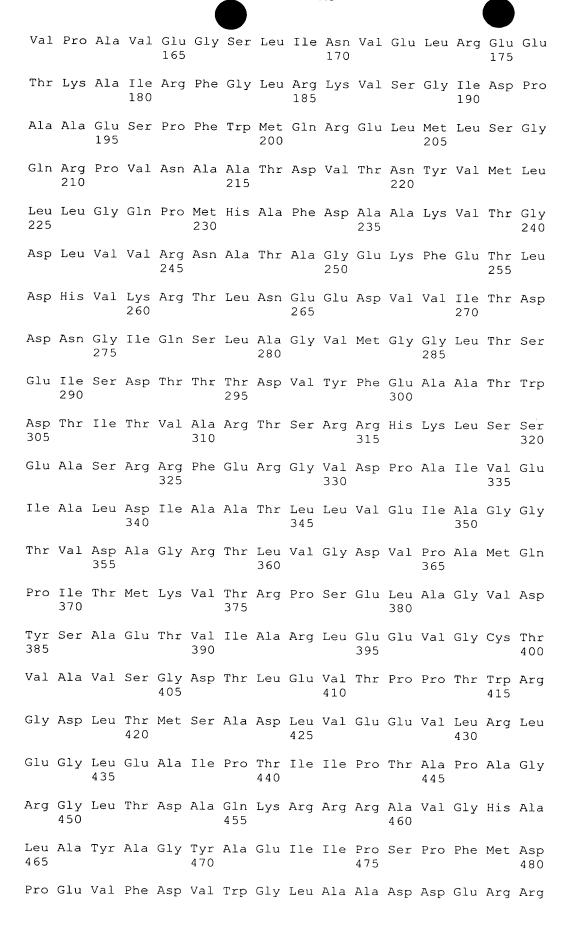
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tcc Ser	gct Ala	gac Asp	ctc Leu 425	gtg Val	gaa Glu	gaa Glu	Val	ctc Leu 430	cgc Arg	ctc Leu	gaa Glu	ggt Gly	ttg Leu 435	gaa Glu	gca Ala	1411
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Ile	Val	Cys 35	Gly	Ala	Arg	Asn	Phe 40	Lys	Glu	Gly	Asp	Thr 45	Val	Val	Val	
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Ser	Tyr	Gly	Glu	Pro	Gly	Glu	Asp	Ala	Arg	Gln	Ala	Leu	Gly	Leu	Glu	

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Arg	Gly 450	Leu	Thr	Asp	Ala	Gln 455	Lys	Arg	Arg	Arg	Ala 460	Val	Gly	His	Ala	
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Ala	Arg 530	Gly	His	Asn	Asp	Phe 535	Ser	Leu	Phe	Gly	Leu 540	Gln	Gln	Val	Ala	
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Leu Ile Glu Thr Val Glu Leu Phe His Val Phe Arg Ser Glu Gln Arg
35 40 45

Gly Glu Asn Lys Lys Ser Leu Ala Phe Ser Leu Arg Phe Arg Ala Ala 50 55 60

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Met Ile Thr Arg Leu

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gcc cca ggt atc tac tcc tgg ttg cca ctg ggt ttg cgc gca gtg cgc 259
Ala Pro Gly Ile Tyr Ser Trp Leu Pro Leu Gly Leu Arg Ala Val Arg
40 45 50

aac att gaa gct gtc gta cgc gag gaa atg gat gcg atc gga gga cag 307

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Glu 70		Lei	u Ph	e Pr	o Th:	г ге	ı Lei	ı Pro	Arg	g Glu 80	ı Pro	Tyr	gaa Glu	a ace	c aca r Thr 85	355
cag Gln	cgt Arg	tgo Trp	g aca	a gaa r Glu 90	ı Tyı	c Gly	gat Asp	tco Ser	g cto Lei 95	ı Ph∈	c cgt Arg	ctg Leu	aaq Lys	g gad s Asp 100	c cgc p Arg	403
aag Lys	ggt Gly	gcc	gad Asp 105	) 1 <b>7</b> 1	c cto	g ctc 1 Leu	gga Gly	cca Pro	Thr	c cac His	gag Glu	gaa Glu	ato Met	Phe	c gcc e Ala	451
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cag a Gln I	. I e (	gag Glu 280	ggc Gly	cgc Arg	gag Glu	Val	acc Thr 285	gca Ala	gat Asp	gac Asp	Thr	ctc ( Leu : 290	aag Lys	tgc Cys	att Ile	979
gtg g Val V	ıtg a 'al I	aag Lys	gtc Val	cgc Arg	gag Glu	cca Pro	ggt Gly	gcc Ala	gaa Glu	gaa ( Glu <i>l</i>	gca ( Ala (	gaa ( Glu 1	ctc Leu	act Thr	gga Gly	1027

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360

Val Val Thr Gly Thr Ser Trp Ile Thr Gly Ala Asp Glu Lys Glu Arg 375 His Val Val Gly Leu Val Ala Gly Arg Asp Phe Thr Pro Asp Gly Phe 395 Ile Glu Ala Ala Glu Ile Lys Glu Gly Asp Pro Ala Pro Ala Gly Glu Gly Thr Leu Thr Leu Ala Arg Gly Ile Glu Ile Gly Ile Ser Ser 420 Ser Ala Ala Ser Thr Pro Lys Pro Ser Thr Ser Lys Ser Trp Thr Lys Thr Ala Ser Ala Pro Ser Gln Pro Trp Ala Leu Arg Ala Arg Cys His Pro Pro Ala Arg Arg Pro Gly Arg Thr Ala Pro Arg 470 <210> 327 <211> 1031 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (94)..(1008) <223> FRXA01938 <400> 327 ccgcgatgag gaacgcccac gcgcaggcgt gctccgcggg acgcgaattt gtgatgaagg 60 attettacte ettegacate tegggatget ggtttg gae gag tee tae gea aag Leu Asp Glu Ser Tyr Ala Lys cac ege gea geg tat eag ege ate ttt gae ege ett gge ttg gaa tae 162 His Arg Ala Ala Tyr Gln Arg Ile Phe Asp Arg Leu Gly Leu Glu Tyr gcc atc tgc cag gca acc tct ggt gcc atg ggc gga tcc gct tcc gag Ala Ile Cys Gln Ala Thr Ser Gly Ala Met Gly Gly Ser Ala Ser Glu 210 gaa ttc ctt gca gta tct gaa aac ggc gaa gat acc ttc gtg cgc tct Glu Phe Leu Ála Val Ser Glu Asn Gly Glu Ásp Thr Phe Val Arg Ser acc tcc ggc aat tac gcc gca aac gtg gaa gct gtt gtt acc cag cca Thr Ser Gly Asn Tyr Ala Ala Asn Val Glu Ala Val Val Thr Gln Pro ggc gtt gag cgt gac atc gaa ggc ctg cca gaa cca gtc acc tac gaa Gly Val Glu Arg Asp Ile Glu Gly Leu Pro Glu Pro Val Thr Tyr Glu 80 act eet gtt tet gaa ace ate gat get ttg gtt gat tgg get aac tee Thr Pro Val Ser Glu Thr Ile Asp Ala Leu Val Asp Trp Ala Asn Ser

atc gac gtg cag atc gag ggc cgc gag gtc acc gca gat gac acc ctc

Ile Asp Val Gln Ile Glu Gly Arg Glu Val Thr Ala Asp Asp Thr Leu

105

	10	5	1 01		e Gi	110	y Arg	3 GTI	ı va.	ı Th:	r Ala 115	a Asp	Asp	o Thi	ctc Leu	450
120	)		···	ı va.	125	o val	. Arç	, GII	l Pro	130	) A VTS	a Glu	ı Glü	ı Ala	gaa Glu 135	498
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ttc ctc cgt gat a Phe Leu Arg Asp A	aac ccg gac o Asn Pro Asp \ 10	gtt gtt cgt o Val Val Arg i 15	gcc tcc cag atc Ala Ser Gln Ile	act cgc 163 Thr Arg 20										
ggc gaa gac ccc g Gly Glu Asp Pro F 25	gcg ctt gtg ( Ala Leu Val <i>I</i>	gac gaa ctg a Asp Glu Leu : 30	att agt gct gat Ile Ser Ala Asp 35	gaa tct 211 Glu Ser										
cgt cgc gaa gca a Arg Arg Glu Ala I 40	itc aag gct o	gcc gac gat 1 Ala Asp Asp 1 45	ttg cgc gct gag Leu Arg Ala Glu 50	cag aag 259 Gln Lys										
gct ttt gga aag a Ala Phe Gly Lys I 55	ag atc gga o Lys Ile Gly ( 60	cag gcc tct ( Gln Ala Ser 1	ccg gag gac cgc Pro Glu Asp Arg 65	cct gca 307 Pro Ala										
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ctc tcc aac gtg g Leu Ser Asn Val V 105	tt tcc ggc g al Ser Gly A	gcg cct gct o Ala Pro Ala o 110	ggt ggc gaa gat Gly Gly Glu Asp 115	gat ttc 451 Asp Phe										
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aag gat cac ctg g Lys Asp His Leu G 135	ag ctc ggt g lu Leu Gly G 140	gaa too oto g Glu Ser Leu G	gga ctt atc gat Gly Leu Ile Asp 145	atg aag 547 Met Lys										
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170 175 180 cgc gaa gct gga ttt agc atg atc cct cca gtt ttg gtg cgc cct 691 Arg Glu Ala Gly Phe Ser Met Met Ile Pro Pro Val Leu Val Arg Pro 185 gaa atc atg gcg ggc act gga ttc ttg ggt gat cac tcc gag gag atc 739 Glu Ile Met Ala Gly Thr Gly Phe Leu Gly Asp His Ser Glu Glu Ile tac tac ctc gaa cgc gat gac atg tac ttg gtg ggt acc tct gag gtg 787 Tyr Tyr Leu Glu Arg Asp Asp Met Tyr Leu Val Gly Thr Ser Glu Val 220 gct ctt gcg ggt tac cac aag gac gaa atc att gat ctc aac gaa ggc 835 Ala Leu Ala Gly Tyr His Lys Asp Glu Ile Ile Asp Leu Asn Glu Gly 235 240 cca gtg aag tac gcc ggt tgg agc tcc tgc ttc cgc cgt gag gct ggt 883 Pro Val Lys Tyr Ala Gly Trp Ser Ser Cys Phe Arg Arg Glu Ala Gly 250 255 tcc tac ggc aag gac acc cga ggc att ttg cgt gtg cac cag ttc gac 931 Ser Tyr Gly Lys Asp Thr Arg Gly Ile Leu Arg Val His Gln Phe Asp aag gtt gag atg ttt gtc tac tgc aag cct gaa gat gct gaa gat gta 979 Lys Val Glu Met Phe Val Tyr Cys Lys Pro Glu Asp Ala Glu Asp Val 280 290 cac cag cag ctg ctc ggc atg gaa aag gaa atg ctc gca gcc atc gag 1027 His Gln Gln Leu Leu Gly Met Glu Lys Glu Met Leu Ala Ala Ile Glu 295 300 gtt cct tac cgc gtc atc gac gtt gcc ggt gga gac ttg ggt gca tct 1075 Val Pro Tyr Arg Val Ile Asp Val Ala Gly Gly Asp Leu Gly Ala Ser 310 315 gct gcc cgc aag ttc gac acc gag gca tgg gtg cca acc cag gac acc 1123 Ala Ala Arg Lys Phe Asp Thr Glu Ala Trp Val Pro Thr Gln Asp Thr 330 340 tac cgt gaa ctc acc tcg acc tct aac tgc acc act ttc cag gct cgt 1171 Tyr Arg Glu Leu Thr Ser Thr Ser Asn Cys Thr Thr Phe Gln Ala Arg 345 350 cgc ctg cag act cgt tac cgc gat gaa aac ggc aag cca cag atc gcc Arg Leu Gln Thr Arg Tyr Arg Asp Glu Asn Gly Lys Pro Gln Ile Ala 360 gca acc ctg aac ggt acg ttg gct acc act cgt tgg ctt gtc gcg atc 1267 Ala Thr Leu Asn Gly Thr Leu Ala Thr Thr Arg Trp Leu Val Ala Ile 375 380 ctg gag aac aac cag cag gcc gat ggc tct gtt gtt gtt cct gag gcg 1315 Leu Glu Asn Asn Gln Gln Ala Asp Gly Ser Val Val Pro Glu Ala 390 395 ctt cgt cca ttc gtg ggc aaa gac gtg ctc aag cca gtg aaa caa gcc Leu Arg Pro Phe Val Gly Lys Asp Val Leu Lys Pro Val Lys Gln Ala

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1389

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<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 330

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Ser Gln Ile Thr Arg Gly Glu Asp Pro Ala Leu Val Asp Glu Leu Ile 20 25 30

Ser Ala Asp Glu Ser Arg Arg Glu Ala Ile Lys Ala Ala Asp Asp Leu 35 40 45

Arg Ala Glu Gln Lys Ala Phe Gly Lys Lys Ile Gly Gln Ala Ser Pro 50 60

Glu Asp Arg Pro Ala Leu Leu Glu Gly Ser Asn Glu Leu Lys Ala Lys 65 70 75 80

Val Lys Asp Ala Glu Ala Ala Gln Glu Ala Ala Glu Ala Lys Val Asn 85 90 95

Glu Leu Gln Met Lys Leu Ser Asn Val Val Ser Gly Ala Pro Ala Gly 100 105 110

Gly Glu Asp Asp Phe Val Val Leu Glu Thr Ile Gly Glu Pro Arg Thr 115 120 125

Phe Asp Phe Glu Pro Lys Asp His Leu Glu Leu Gly Glu Ser Leu Gly 130 135 140

Leu Ile Asp Met Lys Arg Gly Thr Lys Val Ser Gly Ala Arg Phe Tyr 145 150 155 160

Tyr Leu Thr Gly Asp Gly Ala Met Leu Gln Leu Gly Met Leu Met Leu 165 170 175

Ala Ala Gln Lys Ala Arg Glu Ala Gly Phe Ser Met Met Ile Pro Pro 180 185 190

Val Leu Val Arg Pro Glu Ile Met Ala Gly Thr Gly Phe Leu Gly Asp 195 200 205

His Ser Glu Glu Ile Tyr Tyr Leu Glu Arg Asp Asp Met Tyr Leu Val 210 215 220

Gly Thr Ser Glu Val Ala Leu Ala Gly Tyr His Lys Asp Glu Ile Ile 225 230 235 240

Asp Leu Asn Glu Gly Pro Val Lys Tyr Ala Gly Trp Ser Ser Cys Phe 245 250 255

Arg Arg Glu Ala Gly Ser Tyr Gly Lys Asp Thr Arg Gly Ile Leu Arg

260 265 270 Val His Gln Phe Asp Lys Val Glu Met Phe Val Tyr Cys Lys Pro Glu 280 285 Asp Ala Glu Asp Val His Gln Gln Leu Leu Gly Met Glu Lys Glu Met 295 Leu Ala Ala Ile Glu Val Pro Tyr Arg Val Ile Asp Val Ala Gly Gly 310 315 Asp Leu Gly Ala Ser Ala Ala Arg Lys Phe Asp Thr Glu Ala Trp Val Pro Thr Gln Asp Thr Tyr Arg Glu Leu Thr Ser Thr Ser Asn Cys Thr 345 Thr Phe Gln Ala Arg Arg Leu Gln Thr Arg Tyr Arg Asp Glu Asn Gly 355 Lys Pro Gln Ile Ala Ala Thr Leu Asn Gly Thr Leu Ala Thr Thr Arg Trp Leu Val Ala Ile Leu Glu Asn Asn Gln Gln Ala Asp Gly Ser Val 385 Val Val Pro Glu Ala Leu Arg Pro Phe Val Gly Lys Asp Val Leu Lys 410 Pro Val Lys Gln Ala Gly 420 <210> 331 <211> 1383 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1360) <223> RXA02167 <400> 331 ggcctatcgc attgacgacg gaattccggt gcttctcatc gacgaagcca ccgagtggac 60 ccccaacaac tagaagtaca tcaaggacat ttttaacacc atg aac atc att gac 115 Met Asn Ile Ile Asp 1 gaa etc tec tgg ege gga etc atc aac eag tec ace gae ett gag gee Glu Leu Ser Trp Arg Gly Leu Ile Asn Gln Ser Thr Asp Leu Glu Ala 10 20 ctt cgc gag gaa gct tca acc ccc atc acc ttg tac tgc gga ttc gac 211 Leu Arg Glu Glu Ala Ser Thr Pro Ile Thr Leu Tyr Cys Gly Phe Asp 25 30 35 cca acc ggt cca tcc ctc cac gca gga cac ctc gtt cca ctg ctc atg Pro Thr Gly Pro Ser Leu His Ala Gly His Leu Val Pro Leu Leu Met 40 45 50

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												ggc Gly				355
												cgc Arg				403
												gca Ala				451
												gtg Val 130				499
											_	ctc Leu	_	_	-	547
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												ctg Leu				643
ttc Phe	ggc Gly	tgc Cys	acc Thr 185	ctg Leu	cag Gln	gta Val	ggt Gly	ggc Gly 190	ggt Gly	gac Asp	cag Gln	tgg Trp	ggc Gly 195	aac Asn	atc Ile	691
												acc Thr 210				739
gca Ala	gtg Val 215	acc Thr	gta Val	cct Pro	ttg Leu	gtt Val 220	acc Thr	gat Asp	tcc Ser	gac Asp	ggc Gly 225	aag Lys	aag Lys	ttc Phe	ggc Gly	787
aag Lys 230	tcc Ser	acc Thr	ggc Gly	ggc Gly	gga Gly 235	agc Ser	ctc Leu	tgg Trp	ttg Leu	gat Asp 240	ccg Pro	gaa Glu	atg Met	acc Thr	agc Ser 245	835
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												gaa Glu				931
												cgc Arg 290				979

					•											
cgt Arg	cgt Arg 295	Leu	gca Ala	cgc Arg	gaa Glu	atg Met 300	Thr	aac Asn	ttg Leu	gtt Val	cac His 305	gga Gly	acc Thr	gaa Glu	gca Ala	1027
acc Thr 310	Glu	gca Ala	gtc Val	gag Glu	ctt Leu 315	gct Ala	gct Ala	caa Gln	gca Ala	ctg Leu 320	ttc Phe	ggc Gly	cgc Arg	gca Ala	gaa Glu 325	1075
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gat Asp 390	tgg Trp	gag Glu	cct Pro	ttc Phe	gct Ala 395	gaa Glu	gat Asp	ctt Leu	ctt Leu	cac His 400	ggt Gly	tca Ser	tgg Trp	cta Leu	gta Val 405	1315
ctg Leu	cgc Arg	cgt Arg	ggc Gly	aag Lys 410	aag Lys	aac Asn	ttc Phe	gca Ala	gga Gly 415	gtt Val	cag Gln	atc Ile	ctc Leu	ggc Gly 420		1360
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Tyr	Cys	Gly 35	Phe	Asp	Pro	Thr	Gly 40	Pro	Ser	Leu	His	Ala 45	Gly	His	Leu	
Val	Pro 50	Leu	Leu	Met	Leu	Arg 55	Arg	Phe	Gln	Gln	Ala 60	Gly	His	Asn	Pro	
Ile 65	Val	Leu	Ala	Gly	Gly 70	Ala	Thr	Gly	Met	Ile 75	Gly	Asp	Pro	Arg	Asp 80	
Val	Gly	Glu	Arg	Thr 85	Met	Asn	Ser	Ala	Asp 90	Thr	Val	Ser	Asp	Trp 95	Ala	
Glu	Arg	Ile	Ser 100	Gly	Gln	Leu		Arg 105	Phe	Val	Asp	Phe	Asp 110	Gly	Glu	

His Ala Ala Arg Leu Val Asn Asn Ala Glu Trp Thr Asn Glu Met Ser 120 Val Val Thr Phe Leu Arg Asp Val Gly Lys His Phe Ser Leu Asn Thr Met Leu Ala Arg Asp Thr Val Lys Arg Arg Leu Glu Ser Asp Gly Ile 150 155 Ser Tyr Thr Glu Phe Ser Tyr Met Leu Leu Gln Ala Asn Asp Tyr Val 170 Glu Leu Asn Lys Arg Phe Gly Cys Thr Leu Gln Val Gly Gly Asp 185 Gln Trp Gly Asn Ile Val Ser Gly Val Asp Leu Asn Arg Arg Val Asn 200 Gly Thr Ser Val His Ala Val Thr Val Pro Leu Val Thr Asp Ser Asp 215 Gly Lys Lys Phe Gly Lys Ser Thr Gly Gly Gly Ser Leu Trp Leu Asp 230 Pro Glu Met Thr Ser Pro Tyr Ala Trp Tyr Gln Tyr Phe Ile Asn Ala 245 Ser Asp Ala Asp Val Ile Arg Tyr Leu Arg Trp Phe Thr Phe Leu Thr 265 Gln Glu Glu Leu Ala Glu Leu Glu Val Glu Val Ala Glu Arg Pro Phe 280 Lys Arg Glu Ala Gln Arg Arg Leu Ala Arg Glu Met Thr Asn Leu Val 295 His Gly Thr Glu Ala Thr Glu Ala Val Glu Leu Ala Ala Gln Ala Leu 310 Phe Gly Arg Ala Glu Leu Arg Asp Leu Asp Glu Lys Thr Leu Ala Ala 325 Ser Val Ser Glu Thr Ala Val Ala Glu Ile Lys Ala Gly Glu Pro Arg 340 Thr Ile Ile Asp Leu Leu Val Ala Ser Gly Leu Ala Asp Ser Lys Gly Ala Ala Lys Arg Ala Val Lys Glu Gly Gly Ala Tyr Val Asn Asn Glu Arg Ile Glu Ser Asp Asp Trp Glu Pro Phe Ala Glu Asp Leu Leu His 395 Gly Ser Trp Leu Val Leu Arg Arg Gly Lys Lys Asn Phe Ala Gly Val 410 Gln Ile Leu Gly

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cac His	tcg Ser 50	Cys	gct Ala	cac His	gtg Val	ctg Leu 55	gca Ala	cag Gln	gct Ala	gtc Val	cag Gln 60	gca Ala	gaa Glu	ttc Phe	cca Pro	192
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Arç	g Ser	Sen 195	a Ala	a Alá	a Tyr	Trp	Arg 200		' Asp	Gln	. Asp	Asn 205		Gly	Leu	
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435 440 445

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gaa Glu 465		t gco y Ala	c gca a Ala	a tto a Pho	e tac e Tyr 470	- GT7	c cct / Pro	aaq D Lys	g at	t tc e Se: 47!	r Va	t caq l Glr	g gca n Ala	a cgo	g gac g Asp 480	1440
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aac Asn 625	ggc	gtg Val	ccc Pro	gtc Val	gat Asp 630	gag Glu	gca Ala	atc Ile	gct Ala	gtg Val 635	att Ile	tct Ser	tcc Ser	tgg Trp	att Ile 640	1920
ggt Gly	gac Asp	cgc Arg	116	aat Asn 645	gat Asp	cag Gln	ccg Pro	Ser	gag Glu 650	gac Asp	tcc Ser	att Ile	gca Ala	gct Ala 655	cgc Arg	1968
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Phe Thr Ala Val Pro Ala Asn Thr Asp Asp Gly Arg Ala Val Ile Arg
35 40 45

His Ser Cys Ala His Val Leu Ala Gln Ala Val Gln Ala Glu Phe Pro 50 55 60

Gly Thr Lys Leu Gly Ile Gly Pro Ala Ile Glu Asn Gly Phe Tyr Tyr 65 70 75 80

Asp Phe Asp Ala Ala Glu Pro Phe Thr Pro Glu Asp Leu Lys Thr Ile 85 90 95

Glu Lys Arg Met Lys Lys Ile Ile Lys Thr Gly Gln Lys Phe Glu Arg 100 105 110

Arg Val Tyr Glu Ser Ala Glu Ala Ala Glu Glu Leu Lys Asn Glu 115 120 125

Pro Tyr Lys Leu Glu Leu Ile Gln Asp Lys Gly Asn Val Asp Pro Asn 130 135 140

Ser Asp Glu Ala Thr Glu Val Gly Ala Gly Glu Leu Thr Ala Tyr Asp 145 150 155 160

Asn Val Asn Pro Arg Thr Ser Glu Val Glu Trp Ser Asp Leu Cys Arg 165 170 175

Gly Pro His Ile Pro Thr Thr Arg Tyr Ile Pro Ala Phe Ala Leu Thr 180 185 190

Arg Ser Ser Ala Ala Tyr Trp Arg Gly Asp Gln Asp Asn Ala Gly Leu 195 200 205

Gln Arg Ile Tyr Gly Thr Ala Trp Glu Asp Lys Glu Ser Leu Asp Ala 210 215 220

Tyr Gln Thr Met Leu Ala Glu Ala Glu Lys Arg Asp His Arg Arg Leu 225 230 235 240

Gly Thr Glu Leu Asp Leu Phe Ser Phe Pro Asp Asp Leu Gly Ser Gly 245 250 255

Leu Pro Val Phe His Pro Asn Gly Gly Ile Val Arg Asn Glu Met Glu 260 265 270

Asp His Ser Arg Arg Arg His Ile Ala Ala Gly Tyr Ser Phe Val Asn 275 280 285

Thr Pro His Ile Thr Lys Gln Asp Leu Phe Glu Arg Ser Gly His Leu 290 295 300

Gly Phe Tyr Lys Asp Gly Met Phe Pro Pro Met Gln Val Asp Ala Glu 310 315 Phe Asp Glu Asp Gly Asn Val Thr Lys Pro Gly Gln Glu Tyr Tyr Leu 325 Lys Pro Met Asn Cys Pro Met His Asn Leu Ile Phe Asp Ser Arg Gly Arg Ser Tyr Arg Glu Leu Pro Leu Arg Leu Phe Glu Phe Gly Asn Val Tyr Arg Tyr Glu Lys Ser Gly Val Ile His Gly Leu Thr Arg Ala Arg Gly Phe Thr Gln Asp Asp Ala His Ile Tyr Cys Thr Glu Asp Gln Leu Glu Ala Glu Leu Thr Ser Val Leu Asp Phe Ile Leu Ser Leu Leu Arg 405 410 Asp Tyr Gly Leu Asp Asp Phe Tyr Leu Glu Leu Ser Thr Arg Asp Pro Lys Lys Ser Val Gly Ser Asp Glu Ile Trp Glu Arg Ser Thr Glu Ile Leu Asn Arg Val Ala Thr Asn Ser Gly Leu Glu Leu Val Pro Asp Pro 455 Glu Gly Ala Ala Phe Tyr Gly Pro Lys Ile Ser Val Gln Ala Arg Asp 470 475 Ala Ile Gly Arg Thr Trp Gln Met Ser Thr Val Gln Leu Asp Phe Asn 485 Met Pro Glu Arg Phe Asn Leu Glu Tyr Thr Ser Ser Asp Gly Ser Lys 505 Gln Gln Pro Ile Met Ile His Arg Ala Leu Phe Gly Ser Ile Glu Arg Phe Phe Gly Val Leu Leu Glu His Tyr Ala Gly Ala Phe Pro Ala Trp 535 Leu Ala Pro His Gln Val Met Gly Ile Pro Val Ala Asp Asp Cys Ile 555 Pro His Leu Glu Thr Ile Thr Ala Gln Leu Arg Glu Lys Gly Ile Arg 570 Ala Asp Val Asp Thr Ser Asp Asp Arg Met Gln Lys Lys Ile Arg Asn His Thr Thr Gly Lys Val Pro Phe Met Leu Leu Ala Gly Ala Arg Asp 600 Val Glu Ala Asn Ala Val Ser Phe Arg Phe Leu Asp Gly Thr Gln Val Asn Gly Val Pro Val Asp Glu Ala Ile Ala Val Ile Ser Ser Trp Ile

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Arg

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Glu Asn Lys Pro Gly Val Ser Asn Leu Leu Val Ile Gln Ser Ala Leu
50 55 60

acg ggt acc tcc atc gat tcg ctt gtc gac ggc tac cag ggc gct ggc 240
Thr Gly Thr Ser Ile Asp Ser Leu Val Asp Gly Tyr Gln Gly Ala Gly
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85 90 95

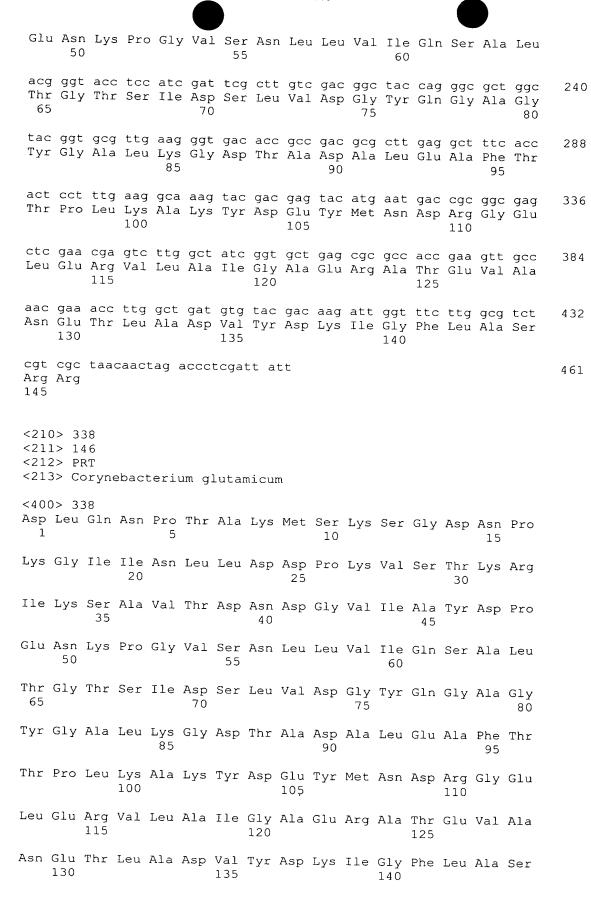
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aco	eggaa	aaag	gtct	gtco	caa g	ıgtga	ictac	ca ct	gata	ıcagc	atg Met 1	Thr	acg Thr	cag Gln	gat Asp 5	115
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GIII	пр	40	ASP	Leu	GIn	Asp	Ser 45	Tyr	Asp	gcc Ala	Phe	Tyr 50	Phe	Ile	Pro	259
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cgc Arg 70	acc Thr	att Ile	tcc Ser	ggc Gly	gcc Ala 75	gca Ala	cag Gln	ctg Leu	ctg Leu	gcc Ala 80	ctg Leu	ggc Gly	att Ile	gat Asp	cca Pro 85	355
	9	501	1111	90	rne	Val	GIN	ser	н1S 95	gtt Val	Pro	Ala	His	Ala 100	Glu	403
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Phe Tyr Phe Ile Pro Asp Leu His Ala Ile Thr Val Asp Gln Glu Pro

Glu Glu Leu Arg Asn Arg Thr Ile Ser Gly Ala Ala Gln Leu Leu Ala 70

Leu Gly Ile Asp Pro Glu Arg Ser Thr Leu Phe Val Gln Ser His Val 85

Pro Ala His Ala Glu Leu Ser Trp Val Leu Thr Cys Leu Thr Gly Phe 100

Gly Glu Ala Ser Arg Met Thr Gln Phe Lys Asp Lys Ser Ser Lys Arg 120

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aaa gat ctc acc gca caa acc gct tcc aga gtc ctt tct gga att cag Lys Asp Leu Thr Ala Gln Thr Ala Ser Arg Val Leu Ser Gly Ile Gln 10 15

ccc Pro	acc Thr	gco Ala	c gat a Asp 25	Ser	tat Tyr	cac His	cto Lei	g ggc 3 Gly 30	' Asr	tac Tyr	ttg Leu	gga Gly	gca Ala	. Val	aag Lys	211
cag Gln	tgg Trp	att Ile 40	Asp	ctg Leu	caa Gln	gat Asp	tco Ser 45	Tyr	gat Asp	gec Ala	ttc Phe	tac Tyr 50	Phe	att Ile	cca Pro	259
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cgc Arg 70	acc Thr	att Ile	tcc Ser	ggc Gly	gcc Ala 75	Ala	cag Gln	ctg Leu	ctg Leu	gcc Ala 80	ctg Leu	ggc Gly	att Ile	gat Asp	cca Pro 85	355
gaa Glu	cgc Arg	tcc Ser	acc Thr	ttg Leu 90	ttt Phe	gtg Val	cag Gln	tcg Ser	cat His 95	gtt Val	ccc Pro	gca Ala	cat His	gca Ala 100	gaa Glu	403
ctg Leu	tca Ser	tgg Trp	gtt Val 105	ctg Leu	acc Thr	tgc Cys	ctg Leu	acc Thr 110	ggt Gly	ttc Phe	ggc Gly	gag Glu	gca Ala 115	tcc Ser	cgc Arg	451
atg Met	acc Thr	cag Gln 120	ttc Phe	aag Lys	gac Asp	aag Lys	tcc Ser 125	tcc Ser	aag Lys	cgt Arg	ggc Gly	gcc Ala 130	gac Asp	cgt Arg	acc Thr	499
tca Ser	gct Ala 135	ggt Gly	ctg Leu	ttc Phe	acc Thr	tac Tyr 140	ccg Pro	atg Met	ctg Leu	atg Met	gca Ala 145	gca Ala	gat Asp	att Ile	ttg Leu	547
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Glu ( 65	Glu 1	Leu .	Arg /	Asn .	Arg 70	Thr	Ile	Ser	Gly .	Ala 75	Ala	Gln	Leu	Leu	Ala 80	
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Pro Ala His Ala Glu Leu Ser Trp Val Leu Thr Cys Leu Thr Gly Phe 100 105 110

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				1	_	5	

gac Asp	cag Gln	aat Asn	aat Asn	gag Glu 10	acc Thr	acc Thr	agc Ser	cag Gln	aac Asn 15	cgc Arg	gca Ala	gac Asp	aag Lys	ctg Leu 20	ccc Pro	163
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gta Val	gac Asp	gcc Ala 40	ggt Gly	tat Tyr	ttc Phe	act Thr	gcc Ala 45	gat Asp	cct Pro	gct Ala	agc Ser	gac Asp 50	aag Lys	cca Pro	gga Gly	259
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					, 5					80					85	

cgc Arg	atg Met	cag Gln	ggc Gly	ttt Phe 90	gag Glu	gtt Val	ttg Leu	tgg Trp	ctg Leu 95	cca Pro	ggt Gly	atg Met	gac Asp	cac His 100	gcg Ala	403
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tg Tr	g ga p Gl 13		g aa p Ly	ıg ca 's Gl	a ga n Gl	a ta u Ty 14	r GT	t gga y Gly	a aa y Ly:	g at s Il	c gg e Gl 14	y Gl	g ca u Gl	g ate n Me	g cgc t Arg	547
gc Al. 15		c gg e Gl	c ga y As	t tc p Se	c gt r Va 15	I AS	c tgo p Trp	g tco Ser	c cgo	g ga g Gl	u Ar	t tto g Phe	c ace	c tto r Lei	g gat ı Asp 165	595
ga As <sub>l</sub>	c ggo c Gly	c tt y Le	g tc u Se	c cg r Ar 17	y Ar	c gto a Val	c caa l Glr	a aco n Thr	175	Phe	c aad e Ly:	g aaq s Lys	g cti Lei	t ttd u Phe 180	gac Asp	643
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cag Gln	acc Thr	ctg Leu	cct Pro 265	1112	cca Pro	ttc Phe	cgc Arg	gat Asp 270	gac Asp	ctg Leu	agc Ser	ctg Leu	aag Lys 275	gtt Val	gtt Val	931
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cgc Arg	gaa Glu	gaa Glu	ctc Leu 345	gca Ala	gcc Ala	cag Gln	GTA.	cgc Arg 350	att Ile	gtc Val	aag Lys	gaa Glu	att Ile 355	cgc Arg	cca Pro	1171

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Sor	- 50	~ A ~	~ 7 ~.	- Di-			_	_								
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<400> 344

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Leu Tyr Gln Gly Trp Val Asp Ala Gly Tyr Phe Thr Ala Asp Pro Ala 35 40 45

Ser Asp Lys Pro Gly Phe Ser Ile Val Leu Pro Pro Pro Asn Val Thr 50 55 60

Gly Gln Leu His Met Gly His Ala Leu Asp His Thr Leu Met Asp Ala 65 70 75 80

Leu Ala Arg Arg Lys Arg Met Gln Gly Phe Glu Val Leu Trp Leu Pro 85 90 95

Gly Met Asp His Ala Gly Ile Ala Thr Gln Thr Lys Val Glu Glu Met 100 105 110

Leu Lys Glu Thr Glu Gly Lys Thr Arg Tyr Asp Tyr Asp Arg Glu Glu 115 120 125

Phe Ile Ala Lys Val Trp Glu Trp Lys Gln Glu Tyr Gly Gly Lys Ile 130 135 140

Gly Glu Gln Met Arg Ala Ile Gly Asp Ser Val Asp Trp Ser Arg Glu 145 150 155 160

Arg Phe Thr Leu Asp Asp Gly Leu Ser Arg Ala Val Gln Thr Ile Phe 165 170 175

Lys Lys Leu Phe Asp Ala Gly Leu Ile Tyr Gln Ala Asn Arg Leu Val 180 185 190

Asn Trp Ser Pro Val Leu Glu Thr Ala Val Ser Asp Ile Glu Val Ile 195 200 205 Tyr Lys Asp Val Glu Gly Glu Leu Val Ser Ile Arg Tyr Gly Ser Leu 215 Asn Asp Asp Glu Pro His Val Ile Val Ala Thr Thr Arg Val Glu Thr 225 230 Met Leu Gly Asp Val Ala Val Ala Val His Pro Asp Asp Glu Arg Tyr Lys Asp Leu Val Gly Gln Thr Leu Pro His Pro Phe Arg Asp Asp Leu Ser Leu Lys Val Val Ala Asp Asp Tyr Val Asp Pro Glu Phe Gly Ser Gly Ala Val Lys Ile Thr Pro Ala His Asp Pro Asn Asp Tyr Ala Leu 290 295 Gly Leu Arg His Asn Leu Asp Met Pro Thr Ile Met Asp Lys Thr Gly 310 315 Arg Ile Ala Asp Thr Gly Thr Gln Phe Asp Gly Leu Thr Arg Glu Glu Ala Arg Ile Lys Val Arg Glu Glu Leu Ala Ala Gln Gly Arg Ile Val 345 Lys Glu Ile Arg Pro Tyr Val His Ser Val Gly His Ser Glu Arg Ser Gly Glu Ala Ile Glu Pro Arg Leu Ser Leu Gln Trp Phe Val Lys Val Glu Glu Leu Ala Lys Met Ser Gly Asp Ala Val Arg Glu Gly Asp Thr Thr Ile His Pro Lys Ser Leu Glu Pro Arg Tyr Phe Asp Trp Val Asp 410 Asn Met His Asp Trp Thr Ile Ser Arg Gln Leu Trp Trp Gly His Arg 425 Ile Pro Ile Trp Tyr Gly Pro Asn Asp Glu Ile Ile Cys Val Gly Pro Asp Glu Gln Ala Pro Glu Gly Tyr Val Gln Asp Pro Asp Val Leu Asp 455 Thr Trp Phe Ser Ser Ala Leu Trp Pro Phe Ser Thr Met Gly Trp Pro Glu Lys Thr Pro Glu Leu Glu Lys Phe Tyr Pro Thr Ser Val Leu Val 490 Thr Ala Tyr Asp Ile Leu Phe Phe Trp Val Ala Arg Met Met Phe Gly Thr Phe Ala Ala Lys Glu Thr Pro Glu Leu Leu Gly Glu Gly Lys

BGI-127CP - 451 -515 520 525 Asp Gly Arg Pro Gln Val Pro Phe Thr Asp Leu Phe Leu His Gly Leu 535 Val Arg Asp Glu His Gly Arg Lys Met Ser Lys Ser Leu Gly Asn Gly Ile Asp Pro Met Asp Trp Val Glu Asn Tyr Gly Ala Asp Ala Leu Arg Phe Thr Leu Ala Arg Gly Ala Asn Pro Gly Val Asp Leu Pro Val Gly Glu Asp Ser Ala Gln Ser Ser Arg Asn Phe Ala Thr Lys Leu Phe Asn 600 Ala Thr Lys Phe Ala Leu Met Asn Gly Ala Val Ser Glu Gly Leu Pro Ala Arg Glu Glu Leu Thr Asp Ala Asp Arg Trp Ile Val Asp Leu Leu Glu Gln Val Arg Leu Asp Val Asp Ala Tyr Leu Asp Asn Tyr Gln Phe 645 665

Ala Lys Ala Asn Glu Glu Leu Tyr His Phe Ala Trp Asn Glu Phe Cys

Asp Trp Tyr Leu Glu Ile Ala Lys Val Gln Ile Pro Arg Glu Gly Thr

Ser Ala Gln Gly Glu Asn Thr Gln Lys Val Leu Gly His Val Leu Asp 695

Ala Leu Leu Arg Leu Leu His Pro Ala Met Pro Phe Val Thr Glu Val

Leu Trp Gln Ala Leu Thr Asp Arg Thr Ser Ile Val Val Ala Ser Trp

Pro Thr Ala Ala Asp Thr Asn Gly Gly Val Ala Val Asp Ala Asp Ala

Ala Arg Arg Ile Gly Asp Val Glu Lys Leu Val Thr Glu Val Arg Arg 760

Phe Arg Ala Asp Gln Gly Val Lys Pro Ser Gln Lys Val Pro Ala Arg

Leu Asp Phe Val Ala Cys Asp Leu Gln Asp Leu Glu Asp Ser Val Arg 795

Ser Leu Val Arg Ile Glu Gln Pro Glu Asp Asp Phe Ala Ala Ser Ala

Ser Leu Glu Ile Arg Leu Ser Gln Ala Thr Ile Thr Val Glu Leu Asp 825

Thr Ser Gly Thr Val Asp Val Ala Ala Glu Arg Lys Arg Leu Glu Lys 840

Asp Leu Ala Asn Ala Gln Lys Glu Leu Glu Thr Thr Ala Lys Lys Leu 850 855 860

Gly Asn Glu Ala Phe Leu Ser Lys Ala Pro Asp Ala Val Val Asp Lys 865 870 875 880

Ile Arg Gly Arg Ala Gln Ile Ala Gln Glu Glu Val Glu Arg Ile Asn 885 890 895

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<211> 590

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<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (96)..(590)

<223> FRXA00985

<400> 345

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- gca ctg ctt cgt ctg ctg cac cca gct atg cct ttc gtc acc gaa gtt Ala Leu Leu Arg Leu Leu His Pro Ala Met Pro Phe Val Thr Glu Val
  10 15 20
- ctg tgg cag gca ctt act gat cgc acc tcc atc gtg gtg gcc tcc tgg 212 Leu Trp Gln Ala Leu Thr Asp Arg Thr Ser Ile Val Val Ala Ser Trp 25 30 35
- cca acc gca gct gac acc aac ggc gga gtc gcc gtg gac gct gat gca 260 Pro Thr Ala Ala Asp Thr Asn Gly Gly Val Ala Val Asp Ala Asp Ala 45 50 55
- gct agg cgc att ggc gac gtc gag aag ctt gtt act gag gtt cgt cgt 308 Ala Arg Arg Ile Gly Asp Val Glu Lys Leu Val Thr Glu Val Arg Arg 60 65 70
- ttc cgc gct gac cag ggt gtg aag cct tcc cag aag gtt cca gca cgc 356
  Phe Arg Ala Asp Gln Gly Val Lys Pro Ser Gln Lys Val Pro Ala Arg
  75 80 85
- ctt gat ttc gtg gca tgt gac ctg cag gat ctg gaa gat tcc gtg cgc 404 Leu Asp Phe Val Ala Cys Asp Leu Gln Asp Leu Glu Asp Ser Val Arg 90 95 100
- tcc ctg gtt cgc atc gag caa cca gaa gat gat ttc gca gct tct gcc Ser Leu Val Arg Ile Glu Gln Pro Glu Asp Asp Phe Ala Ala Ser Ala 105
- agc ctg gag atc cgc ctg agc caa gca acc atc acg gtg gag ctt gac 500 Ser Leu Glu Ile Arg Leu Ser Gln Ala Thr Ile Thr Val Glu Leu Asp

120 125 130 135

acc tct gga act gtt gac gtt gca gca gag cgc aag cgc ctg gaa aag 548
Thr Ser Gly Thr Val Asp Val Ala Ala Glu Arg Lys Arg Leu Glu Lys
140 145 150

gac ctg gct aac gca cag aag gaa ttg gaa acc acc gca aag 590 Asp Leu Ala Asn Ala Gln Lys Glu Leu Glu Thr Thr Ala Lys 155 160 165

<210> 346

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 346

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Ser Ile Val Val Ala Ser Trp Pro Thr Ala Ala Asp Thr Asn Gly Gly  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Val Ala Val Asp Ala Asp Ala Ala Arg Arg Ile Gly Asp Val Glu Lys 50 55 60

Leu Val Thr Glu Val Arg Arg Phe Arg Ala Asp Gln Gly Val Lys Pro 65 70 75 80

Ser Gln Lys Val Pro Ala Arg Leu Asp Phe Val Ala Cys Asp Leu Gln 85 90 95

Asp Leu Glu Asp Ser Val Arg Ser Leu Val Arg Ile Glu Gln Pro Glu 100 105 110

Asp Asp Phe Ala Ala Ser Ala Ser Leu Glu Ile Arg Leu Ser Gln Ala 115 120 125

Thr Ile Thr Val Glu Leu Asp Thr Ser Gly Thr Val Asp Val Ala Ala 130 135 140

Glu Thr Thr Ala Lys

<210> 347

<211> 2149

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<213> Corynebacterium glutamicum

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<223> FRXA01347

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215 220 225 cat gtc att gtt gcc acc cgt gtg gaa acc atg ctc ggc gac gtc 835 His Val Ile Val Ala Thr Thr Arg Val Glu Thr Met Leu Gly Asp Val gct gtt gcc gtg cac cca gac gat gag cgc tac aag gat ttg gtc gga 883 Ala Val Ala Val His Pro Asp Asp Glu Arg Tyr Lys Asp Leu Val Gly 255 cag acc ctg cct cac cca ttc cgc gat gac ctg agc ctg aag gtt gtt 931 Gln Thr Leu Pro His Pro Phe Arg Asp Asp Leu Ser Leu Lys Val Val 265 270 gct gat gat tac gtc gac cca gag ttc ggc tcc ggt gcc gtc aag atc 979 Ála Ásp Ásp Tyr Val Ásp Pro Glu Phe Gly Ser Gly Ála Val Lys Ile 280 acc cca gca cac gac cct aat gac tac gct ctt ggc ctg cgc cac aac 1027 Thr Pro Ala His Asp Pro Asn Asp Tyr Ala Leu Gly Leu Arg His Asn 295 300 ctg gac atg cct acc atc atg gac aag acc gga cgc att gcc gat acc 1075 Leu Asp Met Pro Thr Ile Met Asp Lys Thr Gly Arg Ile Ala Asp Thr 310 320 gga acc cag ttt gat ggc ctg acc cgc gaa gaa gca cgc atc aag gtc 1123 Gly Thr Gln Phe Asp Gly Leu Thr Arg Glu Glu Ala Arg Ile Lys Val 330 335 cgc gaa gaa ctc gca gcc cag ggt cgc att gtc aag gaa att cgc cca 1171 Arg Glu Glu Leu Ala Ala Gln Gly Arg Ile Val Lys Glu Ile Arg Pro 345 350 tac gtc cac tcc gtc gga cac tcc gag cgt tcc ggc gaa gct att gag 1219 Tyr Val His Ser Val Gly His Ser Glu Arg Ser Gly Glu Ala Ile Glu 360 370 cct cgt ctg tct ctg cag tgg ttc gtc aag gtc gaa gag ctg gcc aag 1267 Pro Arg Leu Ser Leu Gln Trp Phe Val Lys Val Glu Glu Leu Ala Lys 375 380 atg tcc ggc gat gcc gtg cgc gaa ggc gac acc acc atc cac ccg aag 1315 Met Ser Gly Asp Ala Val Arg Glu Gly Asp Thr Thr Ile His Pro Lys 390 395 tcc ctg gag cct cgc tac ttt gac tgg gtt gac aac atg cat gac tgg 1363 Ser Leu Glu Pro Arg Tyr Phe Asp Trp Val Asp Asn Met His Asp Trp 410 415 acc att tcc cgt cag ctg tgg tgg gga cac cgc atc cca att tgg tat 1411 Thr Ile Ser Arg Gln Leu Trp Trp Gly His Arg Ile Pro Ile Trp Tyr 425 gga cca aac gat gaa atc atc tgc gtt ggg cct gat gag cag gca cct 1459 Gly Pro Asn Asp Glu Ile Ile Cys Val Gly Pro Asp Glu Gln Ala Pro 440 gag ggc tac gtc caa gac cca gat gtt cta gat acc tgg ttc tct tct 1507 Glu Gly Tyr Val Gln Asp Pro Asp Val Leu Asp Thr Trp Phe Ser Ser 455

gcq Ala 470	ı rec	g tgo ı Trp	g cca Pro	ttt Phe	tct Ser 475	Thr	atg Met	ggt Gly	tgg Trp	cca Pro 480	o Glu	aag Lys	acc Thr	c cct	gag Glu 485	1555
cto Lei	g gag ı Glu	ı aaçı Lys	ttc Phe	tac Tyr 490	Pro	acc Thr	tcc Ser	gtg Val	Leu 495	gtc Val	acc Thr	gcc Ala	tac Tyr	gac Asp 500	atc Ile	1603
ctg Leu	ttc Phe	ttc Phe	tgg Trp 505	٧al	gcc Ala	cgc Arg	atg Met	atg Met 510	Met	ttc Phe	ggc Gly	acc Thr	ttt Phe 515	Ala	gcc Ala	1651
aag Lys	gaa Glu	acc Thr 520	Pro	gaa Glu	ctt Leu	ctg Leu	ggc Gly 525	gaa Glu	ggc Gly	aag Lys	gat Asp	gga Gly 530	cgc Arg	cca Pro	cag Gln	1699
gtt Val	cca Pro 535	ttc Phe	acc Thr	gac Asp	ctc Leu	ttc Phe 540	ctg Leu	cac His	ggc Gly	ctg Leu	gtt Val 545	cgc Arg	gat Asp	gag Glu	cac His	1747
ggc Gly 550	cgc Arg	aag Lys	atg Met	tcc Ser	aag Lys 555	tct Ser	ttg Leu	ggc Gly	aac Asn	ggc Gly 560	atc Ile	gat Asp	ccg Pro	atg Met	gat Asp 565	1795
tgg Trp	gtg Val	gag Glu	aac Asn	tac Tyr 570	ggc Gly	gcg Ala	gat Asp	gcg Ala	ttg Leu 575	cgc Arg	ttc Phe	acc Thr	ctt Leu	gcc Ala 580	cgt Arg	1843
ggc Gly	gct Ala	aac Asn	cca Pro 585	ggc Gly	gtc Val	gac Asp	ctg Leu	cct Pro 590	gtc Val	ggt Gly	gaa Glu	gac Asp	tct Ser 595	gca Ala	cag Gln	1891
agc Ser	tcc Ser	cgt Arg 600	aac Asn	ttt Phe	gcc Ala	acc Thr	aag Lys 605	ctg Leu	ttc Phe	aac Asn	gca Ala	acc Thr 610	aag Lys	ttt Phe	gcg Ala	1939
ctg Leu	atg Met 615	aac Asn	ggt Gly	gca Ala	gtg Val	tcc Ser 620	gaa Glu	ggc Gly	ctg Leu	cca Pro	gca Ala 625	cgt Arg	gaa Glu	gaa Glu	ctc Leu	1987
acc Thr 630	gac Asp	gct Ala	gac Asp	cgc Arg	tgg Trp 635	atc Ile	gtg Val	gac Asp	ctc Leu	ctt Leu 640	gag Glu	cag Gln	gtt Val	cgc Arg	ctc Leu 645	2035
gac Asp	gtt Val	gat Asp	Ата	tac Tyr 650	ctg Leu	gac Asp	aac Asn	tac Tyr	cag Gln 655	ttc Phe	gcg Ala	aag Lys	gcc Ala	aac Asn 660	gag Glu	2083
gag Glu	ctc Leu	tac Tyr	cac His 665	ttt Phe	gcg Ala	tgg Trp	Asn	gag Glu 670	ttc Phe	tgt Cys	gac Asp	tgg Trp	tac Tyr 675	ctg Leu	gaa Glu	2131
atc Ile	gcg Ala	aag Lys 680	gtt ( Val (	cag Gln	atc Ile											2149
<b>~210</b>	> 24	0														`

<210> 348 <211> 683 <212> PRT

<213> Corynebacterium glutamicum

<400> 348

Met Val Cys Val Thr Asp Gln Asn Asn Glu Thr Thr Ser Gln Asn Arg  $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$ 

Ala Asp Lys Leu Pro Lys Ser Trp Asp Pro Lys Ala Val Glu Ala Asp 20 25 30

Leu Tyr Gln Gly Trp Val Asp Ala Gly Tyr Phe Thr Ala Asp Pro Ala 35 40 45

Ser Asp Lys Pro Gly Phe Ser Ile Val Leu Pro Pro Pro Asn Val Thr 50 55 60

Gly Gln Leu His Met Gly His Ala Leu Asp His Thr Leu Met Asp Ala 65 70 75 80

Leu Ala Arg Arg Lys Arg Met Gln Gly Phe Glu Val Leu Trp Leu Pro
85 90 95

Gly Met Asp His Ala Gly Ile Ala Thr Gln Thr Lys Val Glu Glu Met 100 105 110

Leu Lys Glu Thr Glu Gly Lys Thr Arg Tyr Asp Tyr Asp Arg Glu Glu 115 120 125

Phe Ile Ala Lys Val Trp Glu Trp Lys Gln Glu Tyr Gly Gly Lys Ile 130 135 140

Gly Glu Gln Met Arg Ala Ile Gly Asp Ser Val Asp Trp Ser Arg Glu 145 150 155 160

Arg Phe Thr Leu Asp Asp Gly Leu Ser Arg Ala Val Gln Thr Ile Phe 165 170 175

Lys Lys Leu Phe Asp Ala Gly Leu Ile Tyr Gln Ala Asn Arg Leu Val 180 185 190

Asn Trp Ser Pro Val Leu Glu Thr Ala Val Ser Asp Ile Glu Val Ile 195 200 205

Tyr Lys Asp Val Glu Gly Glu Leu Val Ser Ile Arg Tyr Gly Ser Leu 210 215 220

Asn Asp Asp Glu Pro His Val Ile Val Ala Thr Thr Arg Val Glu Thr 225 235 235

Met Leu Gly Asp Val Ala Val Ala Val His Pro Asp Asp Glu Arg Tyr 245 255

Lys Asp Leu Val Gly Gln Thr Leu Pro His Pro Phe Arg Asp Asp Leu 260 265 270

Ser Leu Lys Val Val Ala Asp Asp Tyr Val Asp Pro Glu Phe Gly Ser 275 280 285

Gly Ala Val Lys Ile Thr Pro Ala His Asp Pro Asn Asp Tyr Ala Leu 290 295 300

Gly Leu Arg His Asn Leu Asp Met Pro Thr Ile Met Asp Lys Thr Gly

305 310 320 Arg Ile Ala Asp Thr Gly Thr Gln Phe Asp Gly Leu Thr Arg Glu Glu Ala Arg Ile Lys Val Arg Glu Glu Leu Ala Ala Gln Gly Arg Ile Val Lys Glu Ile Arg Pro Tyr Val His Ser Val Gly His Ser Glu Arg Ser Gly Glu Ala Ile Glu Pro Arg Leu Ser Leu Gln Trp Phe Val Lys Val 375 Glu Glu Leu Ala Lys Met Ser Gly Asp Ala Val Arg Glu Gly Asp Thr 395 Thr Ile His Pro Lys Ser Leu Glu Pro Arg Tyr Phe Asp Trp Val Asp 410 Asn Met His Asp Trp Thr Ile Ser Arg Gln Leu Trp Trp Gly His Arg Ile Pro Ile Trp Tyr Gly Pro Asn Asp Glu Ile Ile Cys Val Gly Pro Asp Glu Gln Ala Pro Glu Gly Tyr Val Gln Asp Pro Asp Val Leu Asp 460 Thr Trp Phe Ser Ser Ala Leu Trp Pro Phe Ser Thr Met Gly Trp Pro 475 Glu Lys Thr Pro Glu Leu Glu Lys Phe Tyr Pro Thr Ser Val Leu Val 490 Thr Ala Tyr Asp Ile Leu Phe Phe Trp Val Ala Arg Met Met Phe Gly Thr Phe Ala Ala Lys Glu Thr Pro Glu Leu Leu Gly Glu Gly Lys Asp Gly Arg Pro Gln Val Pro Phe Thr Asp Leu Phe Leu His Gly Leu Val Arg Asp Glu His Gly Arg Lys Met Ser Lys Ser Leu Gly Asn Gly Ile Asp Pro Met Asp Trp Val Glu Asn Tyr Gly Ala Asp Ala Leu Arg Phe Thr Leu Ala Arg Gly Ala Asn Pro Gly Val Asp Leu Pro Val Gly Glu Asp Ser Ala Gln Ser Ser Arg Asn Phe Ala Thr Lys Leu Phe Asn Ala Thr Lys Phe Ala Leu Met Asn Gly Ala Val Ser Glu Gly Leu Pro Ala Arg Glu Glu Leu Thr Asp Ala Asp Arg Trp Ile Val Asp Leu Leu 635

Glu Gln Val Arg Leu Asp Val Asp Ala Tyr Leu Asp Asn Tyr Gln Phe 645  $\phantom{0}650$   $\phantom{0}655$ 

Ala Lys Ala Asn Glu Glu Leu Tyr His Phe Ala Trp Asn Glu Phe Cys 660 665 670

Asp Trp Tyr Leu Glu Ile Ala Lys Val Gln Ile 675 680

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<222> (101)..(1393)

<223> RXN00454

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				1				5	

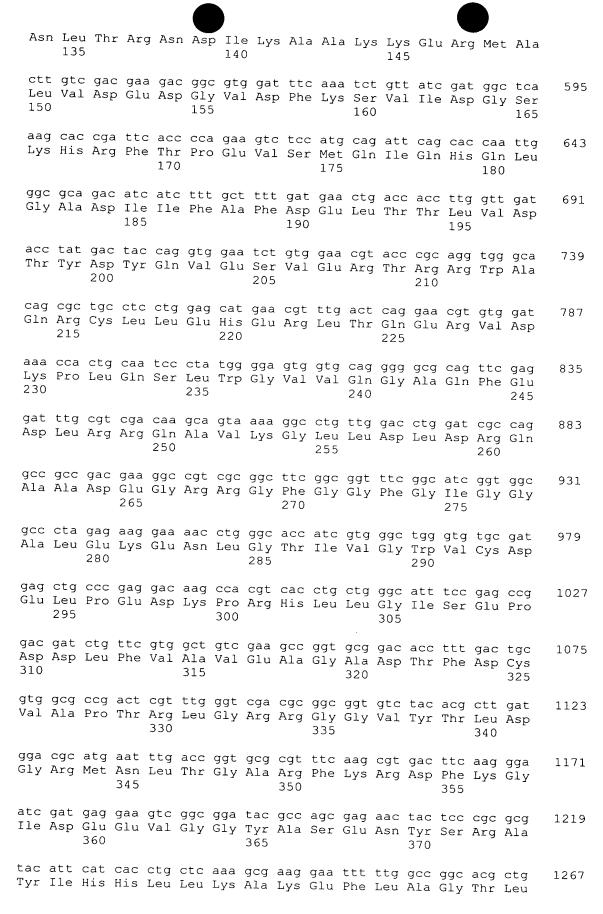
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  Gly Cys Thr Leu Asp Leu Ala Pro Met Ser Asp Leu Ser Phe Thr Leu

  10

  15
- aac aac aag ctt gcc gat gac gcc ccc ggc aag cat ggt cgt aca ggt 211
  Asn Asn Lys Leu Ala Asp Asp Ala Pro Gly Lys His Gly Arg Thr Gly
  25 30 35
- gta atc cac aca cct cac ggt gat att gcc acc cct gct ttc att cct Val Ile His Thr Pro His Gly Asp Ile Ala Thr Pro Ala Phe Ile Pro 40 45 50
- gtg gct acc aaa gcc acg gtg aaa acc ctt acc cct gag cag att cgg 307 Val Ala Thr Lys Ala Thr Val Lys Thr Leu Thr Pro Glu Gln Ile Arg
- gag acc ggc gca cag gct att ttg tcc aac gcc tac cac ctg tat ctg
  Glu Thr Gly Ala Gln Ala Ile Leu Ser Asn Ala Tyr His Leu Tyr Leu
  75 80 85
- cag cct ggc ccc gac atc gtg gac gag gct ggc ggt gtg tct gcc ttt Gln Pro Gly Pro Asp Ile Val Asp Glu Ala Gly Gly Val Ser Ala Phe
  90 95
- gag aac tgg cac ggc ccc acc tac acc gac tcc ggc gga ttc cag gtc Glu Asn Trp His Gly Pro Thr Tyr Thr Asp Ser Gly Gly Phe Gln Val
- atg agc ctg ggc tcc ggc ttt aaa aag gtg ctg gcc atg gac acc acc 499 Met Ser Leu Gly Ser Gly Phe Lys Lys Val Leu Ala Met Asp Thr Thr 120 125 130

aac ttg acg cgc aac gat atc aag gcg gct aaa aaa gag cgc atg gcg 547



375 380 385 tgc acc atg cac aat ctg cac ttc atg atc acc ttg gtg gat aag att Cys Thr Met His Asn Leu His Phe Met Ile Thr Leu Val Asp Lys Ile 390 395 cgt gcc agc atc gat gat ggc acg tac tac gaa ttc aag gaa gaa ttc 1363 Arg Ala Ser Ile Asp Asp Gly Thr Tyr Tyr Glu Phe Lys Glu Glu Phe 410 tta ggc cgg tac tac gcg tcg aag gtt tca taaccttcgc ggcgtttcac 1413 Leu Gly Arg Tyr Tyr Ala Ser Lys Val Ser cca 1416 <210> 350 <211> 431 <212> PRT <213> Corynebacterium glutamicum <400> 350 Met Gly Gly Glu Ala Gly Cys Thr Leu Asp Leu Ala Pro Met Ser Asp Leu Ser Phe Thr Leu Asn Asn Lys Leu Ala Asp Asp Ala Pro Gly Lys His Gly Arg Thr Gly Val Ile His Thr Pro His Gly Asp Ile Ala Thr Pro Ala Phe Ile Pro Val Ala Thr Lys Ala Thr Val Lys Thr Leu Thr Pro Glu Gln Ile Arg Glu Thr Gly Ala Gln Ala Ile Leu Ser Asn Ala Tyr His Leu Tyr Leu Gln Pro Gly Pro Asp Ile Val Asp Glu Ala Gly Gly Val Ser Ala Phe Glu Asn Trp His Gly Pro Thr Tyr Thr Asp Ser Gly Gly Phe Gln Val Met Ser Leu Gly Ser Gly Phe Lys Lys Val Leu Ala Met Asp Thr Thr Asn Leu Thr Arg Asn Asp Ile Lys Ala Ala Lys 135 Lys Glu Arg Met Ala Leu Val Asp Glu Asp Gly Val Asp Phe Lys Ser 150 155 Val Ile Asp Gly Ser Lys His Arg Phe Thr Pro Glu Val Ser Met Gln 165 Ile Gln His Gln Leu Gly Ala Asp Ile Ile Phe Ala Phe Asp Glu Leu 185 Thr Thr Leu Val Asp Thr Tyr Asp Tyr Gln Val Glu Ser Val Glu Arg 200

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Thr Tyr Thr Asp Ser Gly Gly Phe Gln Val Met Ser Leu Gly Ser Gly 65 70 75 80

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Ile Lys Ala Ala Lys Lys Glu Arg Met Ala Leu Val Asp Glu Asp Gly
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Glu Val Ser Met Gln Ile Gln His Gln Leu Gly Ala Asp Ile Ile Phe 130 135 140

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Glu Ser Val Glu Arg Thr Arg Arg Trp Ala Gln Arg Cys Leu Leu Glu 165 170 175

His Glu Arg Leu Thr Gln Glu Arg Val Asp Lys Pro Leu Gln Ser Leu 180 185 190

Trp Gly Val Val Gln Gly Ala Gln Phe Glu Asp Leu Arg Arg Gln Ala 195 200 205

Val Lys Gly Leu Leu Asp Leu Asp Arg Gln Ala Ala Asp Glu Gly Arg 210 215 220

Arg Gly Phe Gly Gly Phe Gly Ile Gly Gly Ala Leu Glu Lys Glu Asn 225 230 235 240

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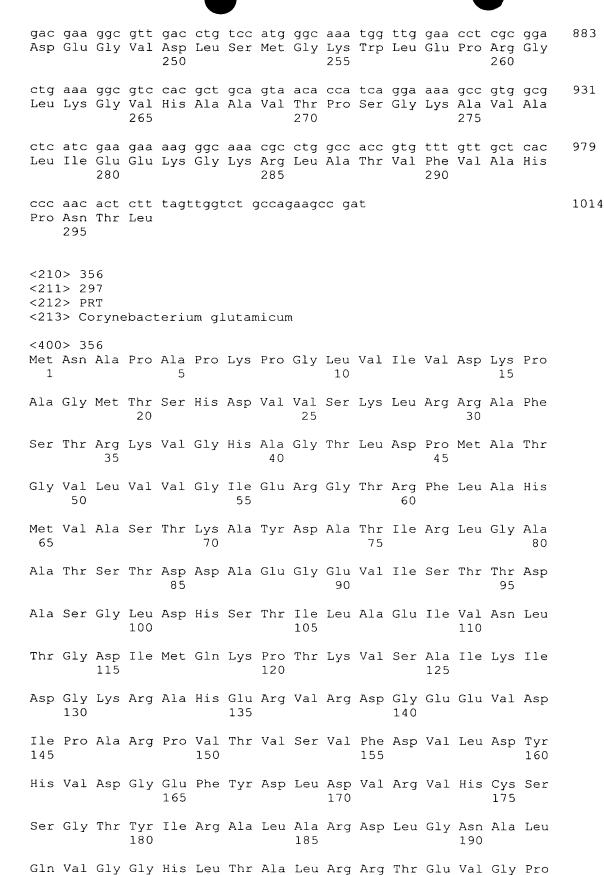
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W

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Thr Arg Val Arg Leu Gly Val Asp Ala Ser Gly Arg Ala Gly Phe Arg
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Ser Arg Val Leu Arg Asp Gln Leu Glu Arg Ile Gly Gly Ile Asp Glu 50 55 60

Leu Pro Glu Phe Glu Leu Gln Asp Leu Glu Pro Thr Ala Gly Trp Arg 65 70 75 80

Thr Arg Val Arg Leu Gly Val Asp Ala Ser Gly Arg Ala Gly Phe Arg 85 90 95

Lys Leu Lys Ser Asn Glu Leu Val Thr Glu Val Ala Cys Ser Gln Val 100 105 110

Val Pro Glu Leu Leu Glu Gly Leu Val Gly Glu Gly Ala Arg Arg Phe 115 120 125

Thr Pro Gly Val Glu Ile Ile Ala Ala Ile Asp Asp Ala Gly Gln Arg 130 135 140

His Val Val Glu Ser Arg Lys Ala Pro Arg Gly Arg Arg Thr Glu Thr 145 150 155 160

Val Leu Lys Val Leu Glu Gly Thr Gly Glu Val Glu Gln Lys Val Gly 165 170 175

Asp Tyr Thr Trp Lys Phe Pro Val Ser Ser Phe Trp Gln Ala His Thr 180 185 190

Lys Ala Pro Ala Ala Tyr Ser Glu Phe Ile Ala Glu Ala Leu Thr Gly 195 200 205

Leu Glu Leu Val Asp Val Asp Lys Arg Gly Pro Val Ala Trp Asp Leu 210 215 220

Tyr Gly Gly Val Gly Leu Phe Ala Pro Ile Ile Thr Ser Lys Leu Gln 225 230 235 240

Ala Ala Val His Ser Val Glu Leu Ser Pro Gly Ser Ala Glu Ala Gly 245 250 255

Glu Glu Ala Leu Ala Gly Leu Pro Val Thr Phe His Thr Gly Arg Val 260 265 270

Glu Gly Met Ala Ser Gln Leu Pro Ser Pro Asn Val Val Leu Asp 275 280 285

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ctt gtg ggt gag ggc gct cgt cgt ttc acc cct ggc gtg gag atc att 144
Leu Val Gly Glu Gly Ala Arg Arg Phe Thr Pro Gly Val Glu Ile Ile

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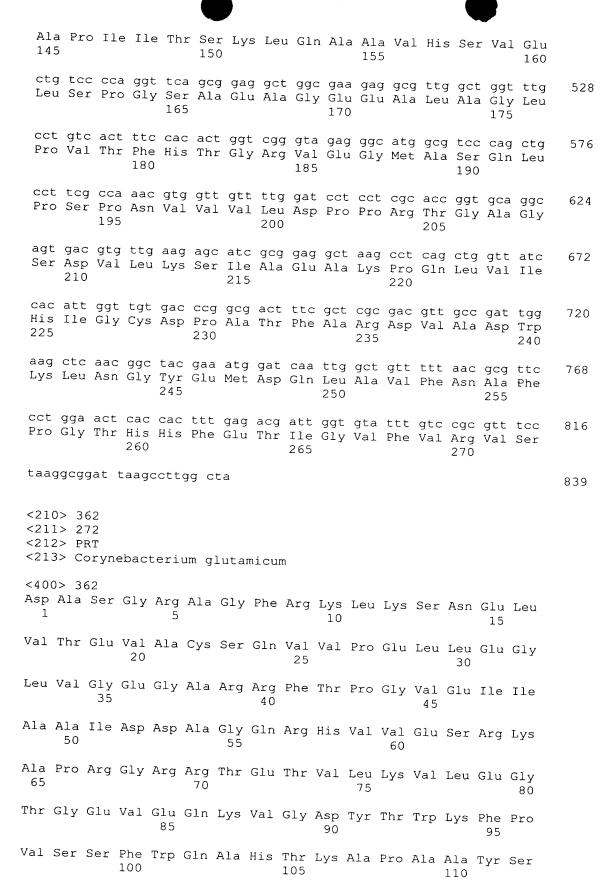
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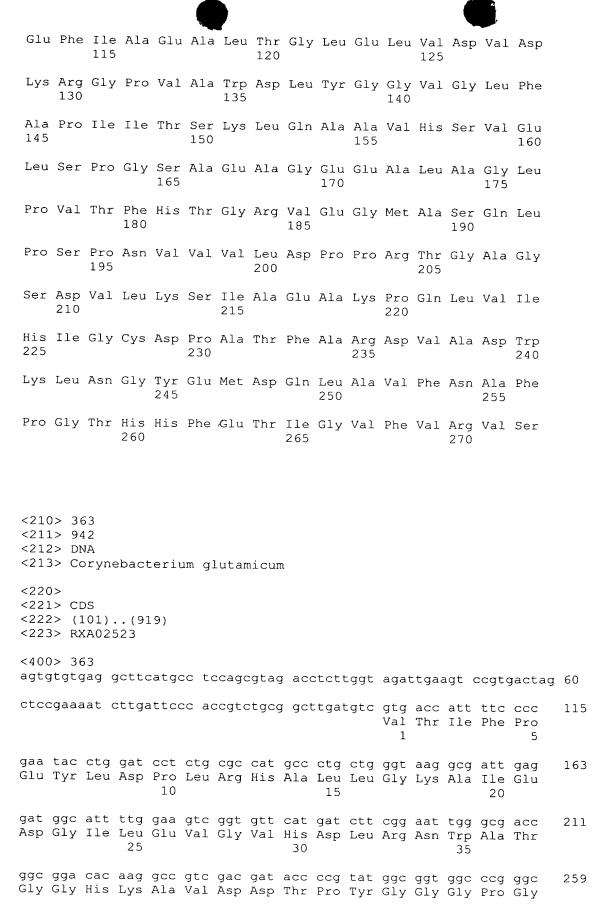
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Leu Asp Asp Val Ala Ala Gly Arg Val Ser Gly Ala Glu Leu Asp Ser 65 70 75 80

Glu Lys Arg Ala Tyr Val Val Glu Glu Asp Arg Asp Leu Pro Leu Leu 100 105 110

Leu Val Pro Thr Pro Ala Gly Lys Pro Phe Thr Gln Ala Asp Ala Gln 115 120 125

Ala Trp Ser Asn Glu Glu His Ile Val Phe Ala Cys Gly Arg Tyr Glu 130 135 140

Gly Ile Asp Gln Arg Val Ile Asp Asp Ala Ala Asn Arg Tyr Arg Val 145 150 155 160

Arg Glu Val Ser Ile Gly Asp Tyr Val Leu Ile Gly Gly Glu Val Ala 165 170 175

Val Leu Val Ile Ala Glu Ala Val Val Arg Leu Ile Pro Gly Val Leu 180 185 190

Gly Asn Arg Arg Ser His Glu Glu Asp Ser Phe Ser Asp Gly Leu Leu 195 200 205

Glu Gly Pro Ser Tyr Thr Lys Pro Arg Thr Trp Arg Gly Leu Asp Val 210 215 220

Pro Glu Val Leu Phe Ser Gly Asn His Ala Lys Val Asp Arg Trp Arg 225 235 240

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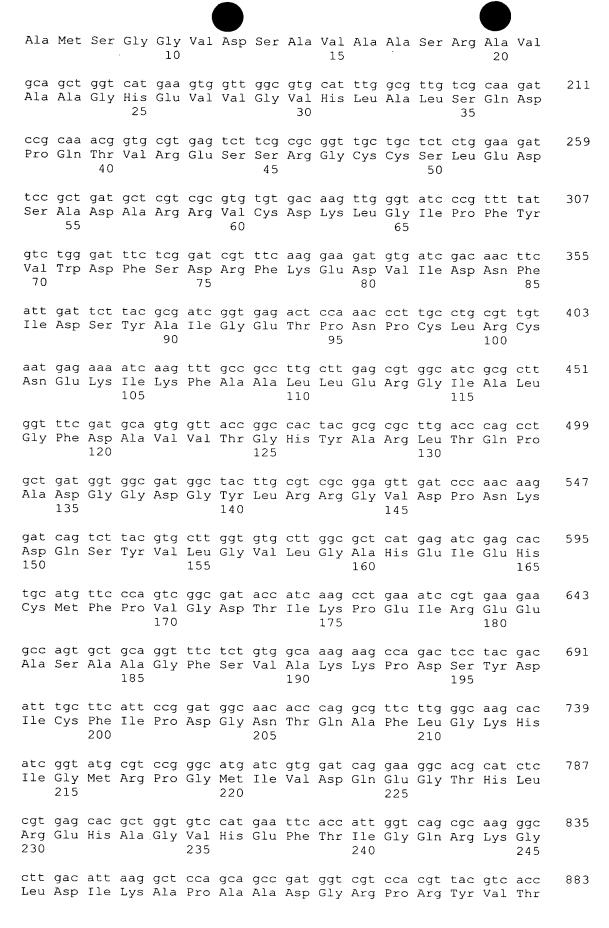
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gca atg agt gga ggc gtt gat tee gee gte geg geg tea ege geg gte

115



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Met Thr Ser Val Ser

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ctg gtt gaa ggc tct gaa aac gag ctg acc aca aag acc gca gag  $\,$  163 Leu Val Glu Gly Ser Glu Asn Glu Leu Thr Thr Lys Thr Ala Ala Glu  $\,$  10  $\,$  15  $\,$  20

ctg gca ggt ctt att cat tcc cgc gag gta act tcc cgc gag gtt act 211 Leu Ala Gly Leu Ile His Ser Arg Glu Val Thr Ser Arg Glu Val Thr 25 30 35

caa gcg cac cta gat cgc att gct gcg gtt gac ggc gat att cat gca 259
Gln Ala His Leu Asp Arg Ile Ala Ala Val Asp Gly Asp Ile His Ala
40 45 50

ttt ctc cac gtt ggc cag gag gac ctg aac gcg gcg gat gac gtc 307 Phe Leu His Val Gly Gln Glu Glu Ala Leu Asn Ala Ala Asp Asp Val

gat aag cgt cta gac gct gga gag gca cct gcc tcg gct ttg gct ggc 355 Asp Lys Arg Leu Asp Ala Gly Glu Ala Pro Ala Ser Ala Leu Ala Gly 70 75 80 85

gtg ccg ctt gcg ctg aag gat gtc ttt acc acc act gat gcg ccg acc 403 Val Pro Leu Ala Leu Lys Asp Val Phe Thr Thr Thr Asp Ala Pro Thr 90 95 100

acg gcg gca tcg aag atg ctt gag ggc tac atg agc cct tat gac gcg 451
Thr Ala Ala Ser Lys Met Leu Glu Gly Tyr Met Ser Pro Tyr Asp Ala
105 110 115

act gtg acc cgc aag atc cgt gag gct ggc atc cca att ttg ggt aag 499
Thr Val Thr Arg Lys Ile Arg Glu Ala Gly Ile Pro Ile Leu Gly Lys
120 125 130

acc aac atg gat gag ttt gcg atg ggt tcc tcc act gag aac tcc gca 547
Thr Asn Met Asp Glu Phe Ala Met Gly Ser Ser Thr Glu Asn Ser Ala
135

tac ggc cca acc cac aat ccg tgg gat ctg gag cgc acc gca ggt ggt 595

Tyr 150	Gly	Pro	Thr	His	Asn 155	Pro	Trp	Asp	Leu	Glu 160	Arg	Thr	Ala	Gly	Gly 165	
	ggt Gly															643
	att Ile			_						_	_		-		_	691
	aac Asn															739
	ctg Leu 215															787
_	act Thr	_	_	-				_			_		_			835
	gct Ala															883
	gct Ala															931
	gtg Val															979
	gca Ala 295					-		_	_	_		_			-	1027
	gtc Val	Glu	Val	Asp		Pro	His	Phe	Āsp	Āsp	Āla	Leu	бĺу	Ala		1075
tac Tyr	ctg Leu	att Ile	ctt Leu	cct Pro 330	tgt Cys	gaa Glu	gtt Val	tcc Ser	tcc Ser 335	aac Asn	ctc Leu	gcg Ala	cgt Arg	ttt Phe 340	gac Asp	1123
	atg Met															1171
	gag Glu															1219
	cgc Arg 375															1267
_	gcg Ala			-	_	_	_	_	-	_				_	_	1315

W W

IJ

- 493 -

Thr Glu Asn Ser Ala Tyr Gly Pro Thr His Asn Pro Trp Asp Leu Glu 145 150 155 Arg Thr Ala Gly Gly Ser Gly Gly Ser Ser Ala Ala Leu Ala Ala 165 170 Gly Gln Ala Pro Leu Ala Ile Gly Thr Asp Thr Gly Gly Ser Ile Arg 185 Gln Pro Ala Ala Leu Thr Asn Thr Val Gly Val Lys Pro Thr Tyr Gly 200 Thr Val Ser Arg Tyr Gly Leu Ile Ala Cys Ala Ser Ser Leu Asp Gln 215 Gly Gly Pro Thr Ala Arg Thr Val Leu Asp Thr Ala Leu Leu His Glu 235 Val Ile Ala Gly His Asp Ala Phe Asp Ala Thr Ser Val Asn Arg Pro Val Ala Pro Val Val Gln Ala Ala Arg Glu Gly Ala Asn Gly Asp Leu 265 Lys Gly Val Lys Val Gly Val Val Lys Gln Phe Asp Arg Asp Gly Tyr Gln Pro Gly Val Leu Glu Ala Phe His Ala Ser Val Glu Gln Met Arg 295 Ser Gln Gly Ala Glu Ile Val Glu Val Asp Cys Pro His Phe Asp Asp Ala Leu Gly Ala Tyr Tyr Leu Ile Leu Pro Cys Glu Val Ser Ser Asn Leu Ala Arg Phe Asp Gly Met Arg Tyr Gly Leu Arg Ala Gly Asp Asp Gly Thr Arg Ser Ala Asp Glu Val Met Ala Tyr Thr Arg Ala Gln Gly Phe Gly Pro Glu Val Lys Arg Arg Ile Ile Leu Gly Thr Tyr Ala Leu Ser Val Gly Tyr Tyr Asp Ala Tyr Tyr Leu Gln Ala Gln Arg Val Arg 395 Thr Leu Ile Ala Gln Asp Phe Ala Lys Ala Tyr Glu Gln Val Asp Ile 410 Leu Val Ser Pro Thr Thr Pro Thr Thr Ala Phe Lys Leu Gly Glu Lys 425 Val Thr Asp Pro Leu Glu Met Tyr Asn Phe Asp Leu Cys Thr Leu Pro Leu Asn Leu Ala Gly Leu Ala Gly Met Ser Leu Pro Ser Gly Leu Ala

Ser Asp Thr Gly Leu Pro Val Gly Leu Gln Leu Met Ala Pro Ala Phe 470 475 Gln Asp Asp Arg Leu Tyr Arg Val Gly Ala Ala Phe Glu Ala Gly Arg 485 490 Lys <210> 375 <211> 420 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(397) <223> RXA00210 <400> 375 tgtccacctc gtgcagtaag ataaaccaac agttgcgcat gcgtgcgcaa gttaaatttt 60 cttgtaccca ttgtgactag cgaagaggat cagaaaccaa gtg cct gag att tcg Val Pro Glu Ile Ser cgc gac cag gtc gct cac ctt gcc aaa ctt tcc aga ctg gcg ctc act Arg Asp Gln Val Ala His Leu Ala Lys Leu Ser Arg Leu Ala Leu Thr 10 gag gaa gaa ctc gag cag ttt gct gga cag atc gat gac att gtc gga 211 Glu Glu Glu Leu Glu Gln Phe Ala Gly Gln Ile Asp Asp Ile Val Gly 30 tat gtt tcc gca gtt caa aac gtc gac gcc gca ggt gtt gag cct atg 259 Tyr Val Ser Ala Val Gln Asn Val Asp Ala Ala Gly Val Glu Pro Met 45 age cae eeg cae age ate gee ace ace atg egt gaa gat gte gtg cae 307 Ser His Pro His Ser Ile Ala Thr Thr Met Arg Glu Asp Val Val His 60 aag acc ctc gat gct gcg gct gcg ttg gac caa gcg ccc gct gtc gag 355 Lys Thr Leu Asp Ala Ala Ala Leu Asp Gln Ala Pro Ala Val Glu 70 75 80 gat gga cgt ttt atg gtt ccg cag att ctg ggt gag ggc gac 397 Asp Gly Arg Phe Met Val Pro Gln Ile Leu Gly Glu Gly Asp 90 taataattat gaccaacaag tac 420 <210> 376 <211> 99

<212> PRT

<213> Corynebacterium glutamicum

<400> 376

Val Pro Glu Ile Ser Arg Asp Gln Val Ala His Leu Ala Lys Leu Ser

1 10 Arg Leu Ala Leu Thr Glu Glu Glu Leu Glu Gln Phe Ala Gly Gln Ile 20 Asp Asp Ile Val Gly Tyr Val Ser Ala Val Gln Asn Val Asp Ala Ala Gly Val Glu Pro Met Ser His Pro His Ser Ile Ala Thr Thr Met Arg Glu Asp Val Val His Lys Thr Leu Asp Ala Ala Ala Leu Asp Gln Ala Pro Ala Val Glu Asp Gly Arg Phe Met Val Pro Gln Ile Leu Gly Glu Gly Asp <210> 377 <211> 1260 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1237) <223> RXA02686 <400> 377 ettetteggt gaaggtteeg geaggeeeea aataggeeae aacagttggt gegtegetea 60 tggttacaca gcttaacccg ccgaactaag gtgggtgtcc atg tct gtt gct caa Met Ser Val Ala Gln 1 tta gcg aac cgc ttg gcc caa ctc tcc ccc gcc gag cat ggt ttt gca 163 Leu Ala Asn Arg Leu Ala Gln Leu Ser Pro Ala Glu His Gly Phe Ala 15 tgg ttc gac cct gaa atc acc gct ggc cat ggc gtt ggc ccg ttg cat 211 Trp Phe Asp Pro Glu Ile Thr Ala Gly His Gly Val Gly Pro Leu His 30 ggc atg gtg att cca gcc aag gac ctc aac gat gtc gca ggc atg ccc 259 Gly Met Val Ile Pro Ala Lys Asp Leu Asn Asp Val Ala Gly Met Pro acc gcg ttc gga aat gca tct cgg cga aag gta gca aca gat acc gat 307 Thr Ala Phe Gly Asn Ala Ser Arg Arg Lys Val Ala Thr Asp Thr Asp 55 60 ccg ttc atc caa aat ctc atc gac cgc ggc gcg atc atc gct ggc aaa Pro Phe Ile Gln Asn Leu Ile Asp Arg Gly Ala Ile Ile Ala Gly Lys 70 75 acc caa acc agc gag ctc ggc atg acg gcg tat tgc gaa ccc atc gac 403

Thr Gln Thr Ser Glu Leu Gly Met Thr Ala Tyr Cys Glu Pro Ile Asp

95

	gac Asp														451
	tcg Ser					-	-	-		_		-	-	-	499
	cac His 135	_	-				_			-		-	-		547
	Gly aaa														595
	tcc Ser														643
-	cac His	_			-			_	_	_			_		691
	gag Glu			-		_		-	_	_			_	_	739
	ctc Leu 215	-		-			_			_			_		787
	tcc Ser	_					-		-		_	-			835
	gtt Val														883
	aca Thr	-	 _	_	_			_	_					_	931
	caa Gln														979
	gca Ala 295														1027
	ccc Pro														1075
	gca Ala														1123

ggt ggt gca gcc atc agc gtg cct gtt gaa ggt gtc ggc att cat ctt Gly Gly Ala Ala Ile Ser Val Pro Val Glu Gly Val Gly Ile His Leu 345 350 ggt ggg ata cgc gta cga gat gaa gac ctc tta gga tta gca gca ttt Gly Gly Ile Arg Val Arg Asp Glu Asp Leu Leu Gly Leu Ala Ala Phe 365 qtq qaa aga qct qtq qca tqagtagttc agtaatgtca ccg Val Glu Arq Ala Val Ala <210> 378 <211> 379 <212> PRT <213> Corynebacterium glutamicum <400> 378 Met Ser Val Ala Gln Leu Ala Asn Arg Leu Ala Gln Leu Ser Pro Ala Glu His Gly Phe Ala Trp Phe Asp Pro Glu Ile Thr Ala Gly His Gly 25 Val Gly Pro Leu His Gly Met Val Ile Pro Ala Lys Asp Leu Asn Asp 35 Val Ala Gly Met Pro Thr Ala Phe Gly Asn Ala Ser Arg Arg Lys Val Ala Thr Asp Thr Asp Pro Phe Ile Gln Asn Leu Ile Asp Arg Gly Ala Ile Ile Ala Gly Lys Thr Gln Thr Ser Glu Leu Gly Met Thr Ala Tyr Cys Glu Pro Ile Asp Met Asp Ala Pro Ser Asn Pro Val Leu Pro Gly 105 100 His Thr Pro Gly Gly Ser Ser Gly Gly Ala Ala Val Ala Val Ala Arg 120 Ser Leu Val Asp Ala Ala His Ala Ser Asp Gly Gly Gly Ser Ile Arg 135 130 Val Pro Ala Ala Ala Cys Gly Leu Val Gly Phe Lys Pro Ala His Asp 155 145 Ser Ser Gly Gly Asn Pro Ser Thr Gln Gly Phe Ile Thr Arg Asp Val 170 165 Ala Thr Gln Val Arg Leu His Ala Leu Gln Pro Arg Thr Arg Arg Leu 185 Arg Ile Gly Val Leu Ala Glu Pro Ile His Ala Asn Ser Leu Val Asp 200 205

Ala Pro Phe Leu Ser Ile Leu Glu Ser Thr Ala His Leu Leu Glu Lys

220

215

210

1171

1219

Ala Gly His Glu Ile Val Ser Val Pro Leu Pro Tyr Gly Ala Trp Ala 230 Phe Asp Ala Tyr Thr Glu Val Phe Met Met Lys Ser Ala Gly Leu Thr 245 Asn Leu Gly Ser Pro Ile Thr Arg Trp Leu Ser Glu Gln Gly Arg Ser Leu Ser Pro Ser Asp Arg Gln Ser Ser Val Lys Ala Phe Asp Ser Val Ala Glu Thr Val His Gly Ala Trp Asp Ile Asp Val Leu Leu Thr Pro Thr Leu Ala Tyr Ala Pro Pro Lys Ile Gly Tyr Phe Ser Ser Met Pro Pro Glu Glu Asp Phe Leu Ala Gln Thr Lys Trp Thr Pro Trp Ala Thr Leu Phe Asn Met Thr Gly Gly Ala Ala Ile Ser Val Pro Val Glu Gly Val Gly Ile His Leu Gly Gly Ile Arg Val Arg Asp Glu Asp Leu Leu Gly Leu Ala Ala Phe Val Glu Arg Ala Val Ala 375 <210> 379 <211> 886 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(886) <223> RXA02625 <400> 379 ctcaattaag cagcaatccg agccggggga gcgctgtcag aaatggaccg tgccacccca 60 115 tgacaacatg cttgcacaat gatgactaga ataatgaccc atg act gca gcc ttt Met Thr Ala Ala Phe 1 163 tat gat ctg atg gac ttc gat gaa gtt cta gag aaa tat gac ccg gtg Tyr Asp Leu Met Asp Phe Asp Glu Val Leu Glu Lys Tyr Asp Pro Val 10 211 atq qqa ctt qaq qtc cac gtc gaa ctg ggc act gag acc aag atg ttc Met Gly Leu Glu Val His Val Glu Leu Gly Thr Glu Thr Lys Met Phe 259 tot goa tot tot goa cac ttt ggc got gaa coc aat agc aat gtt gac Ser Ala Ser Ser Ala His Phe Gly Ala Glu Pro Asn Ser Asn Val Asp 45 cca gtt tct ttg ggt ctc cca ggc gca ctt cct gtg gtt aac gcc aag

Pro	Val 55	Ser	Leu	Gly	Leu	Pro 60	Gly	Ala	Leu	Pro	Val 65	Val	Asn	Ala	Lys	
					att Ile 75											355
					ttt Phe											403
					atc Ile											451
ggc Gly	tac Tyr	ctg Leu 120	gat Asp	gtt Val	gtt Val	ctg Leu	gag Glu 125	gac Asp	ggc Gly	acc Thr	gag Glu	tgg Trp 130	cgt Arg	gtg Val	gaa Glu	499
atc Ile	gaa Glu 135	cgc Arg	gct Ala	cac His	atg Met	gag Glu 140	gaa Glu	gac Asp	acc Thr	gga Gly	aag Lys 145	ctc Leu	acc Thr	cac His	ctg Leu	547
					cgt Arg 155											595
tgc Cys	aac Asn	cgt Arg	gca Ala	ggc Gly 170	gtc Val	cct Pro	ttg Leu	att Ile	gag Glu 175	gtt Val	gtc Val	acc Thr	aag Lys	cca Pro 180	atc Ile	643
					cgc Arg											691
					gtt Val											739
					cgt Arg											787
					ggc Gly 235											835
					cag Gln											883
cag Gln																886

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